GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.9581 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-29
Perfect score: 2462
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWAECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2408	97.8	467	4	US-09-273-871A-9	Sequence 9, Appli
2	2282	92.7	441	3	US-09-121-425-1	Sequence 1, Appli
3	2282	92.7	441	4	US-09-634-493A-1	Sequence 1, Appli
4	2270	92.2	467	3	US-09-121-425-2	Sequence 2, Appli
5	2270	92.2	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1879	76.3	467	1	US-07-923-724-8	Sequence 8, Appli
7	1879	76.3	467	2	US-08-609-426A-8	Sequence 8, Appli
8	1879	76.3	467	2	US-08-374-652C-2	Sequence 2, Appli
9	1875	76.2	467	1	US-08-151-574-32	Sequence 32, Appl
10	1875	76.2	467	1	US-08-146-424-20	Sequence 20, Appl
11	1875	76.2	467	1	US-08-693-709-2	Sequence 2, Appli
12	1875	76.2	467	2	US-08-419-448-32	Sequence 32, Appl
13	1875	76.2	467	2	US-08-819-825-3	Sequence 3, Appli
14	1875	76.2	467	3	US-09-163-642-3	Sequence 3, Appli
15	1875	76.2	467	4	US-09-233-510-32	Sequence 32, Appl
16	1875	76.2	467	4	US-09-636-499-5	Sequence 5, Appli
17	1867	75.8	465	3	US-08-868-435-33	Sequence 33, Appl
18	1867	75.8	465	4	US-08-744-231-33	Sequence 33, Appl
19	1867	75.8	465	4	US-09-044-718-78	Sequence 78, Appl
20	1867	75.8	465	4	US-09-636-499-6	Sequence 6, Appli
21	1867	75.8	465	4	US-09-273-871A-8	Sequence 8, Appli
22	1863	75.7	467	4	US-09-273-871A-11	Sequence 11, Appl
23	1860	75.5	467	3	US-09-155-855-3	Sequence 3, Appli
24	1860	75.5	467	4	US-09-543-744-3	Sequence 3, Appli
25	1860	75.5	467	4	US-09-929-060-3	Sequence 3, Appli
26	1859	75.5	465	4	US-09-044-718-80	Sequence 80, Appl
27	1858	75.5	465	4	US-09-044-718-79	Sequence 79, Appl
28	1857.5	75.4	439	4	US-09-044-718-3	Sequence 3, Appli
29	1857.5	75.4	449	4	US-09-044-718-12	Sequence 12, Appl
30	1855	75.3	465	4	US-09-044-718-81	Sequence 81, Appl
31	1851	75.2	462	4	US-09-636-499-12	Sequence 12, Appl
32	1845	74.9	469	4	US-09-044-718-82	Sequence 82, Appl
33	1839	74.7	466	3	US-08-868-435-35	Sequence 35, Appl
34	1839	74.7	466	4	US-08-744-231-35	Sequence 35, Appl
35	1835.5	74.6	463	3	US-08-868-435-29	Sequence 29, Appl
36	1835.5	74.6	463	4	US-08-744-231-29	Sequence 29, Appl
37	1835.5	74.6	463	4	US-09-273-871A-10	Sequence 10, Appl
38	1833	74.5	444	4	US-09-044-718-1	Sequence 1, Appli
39	1820.5	73.9	447	4	US-09-044-718-6	Sequence 6, Appli
40	1818	73.8	443	3	US-09-155-855-1	Sequence 1, Appli
41	1818	73.8	443	4	US-09-543-744-1	Sequence 1, Appli
42	1818	73.8	443	4	US-09-929-060-1	Sequence 1, Appli
43	1813	73.6	443	3	US-09-155-855-2	Sequence 2, Appli
44	1813	73.6	443	4	US-09-543-744-2	Sequence 2, Appli
45	1813	73.6	443	4	US-09-929-060-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Query Match 97.8%; Score 2408; DB 4; Length 467;
Best Local Similarity 97.9%; Pred. No. 1.9e-243;
Matches 457; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
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Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
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              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||| ||||||||
Db        241 ARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLG 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
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              |||:|||||||||||||| |||||||||||||||||||||||| ||||||||||||||||
Db        361 HDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQAEKEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
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Db        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467


RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

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  Best Local Similarity   97.7%;  Pred. No. 2.8e-230;
  Matches  431;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          27 NSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARY 86
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Db           1 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 60

Qy          87 PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 146
               |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 PTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

Qy         147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGY 206
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Db         121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy         207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVILTDEDVVYLMDMCPF 266
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Db         181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

Qy         267 DTVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 326
               :|||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
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Qy         327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 386
               || ||||||||||||||||||||||||||||||||:|||||||||||||| |||||||
Db         301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy         387 ESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 446
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Db         361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy         447 DDFVEGLSFARSGGNWAECFA 467
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Db         421 DDFVEGLSFARSGGNWAECFA 441


RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-1

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  Best Local Similarity   97.7%;  Pred. No. 2.8e-230;
  Matches  431;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          27 NSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARY 86
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Db           1 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 60

Qy          87 PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 146
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Qy         147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGY 206
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Db         121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy         207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 266
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Qy         267 DTVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 326
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Db         241 ETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300

Qy         327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 386
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Db         301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy         387 ESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 446
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Db         361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy         447 DDFVEGLSFARSGGNWAECFA 467
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Db         421 DDFVEGLSFARSGGNWAECFA 441


RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
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;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 467
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:consensus
;    OTHER INFORMATION: sequence
US-09-121-425-2

  Query Match             92.2%;  Score 2270;  DB 3;  Length 467;
  Best Local Similarity   89.7%;  Pred. No. 5.5e-229;
  Matches  437;  Conservative    3;  Mismatches    7;  Indels   40;  Gaps    2;

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Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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Db        101 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160

Qy        181 KLADPGSQPHQASPVIN-------------------VIIPEGSGYNNTLDHGTCTAFED 220
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Db        161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy        221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSP 280
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Db        221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

Qy        281 FCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
              |||||||||| ||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy        341 TLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWT 400
              |||||||||||||||||||||||:||||||||||||| ||||||||||||||||||||||
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Qy        401 VPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460

Qy        461 NWAECFA 467
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Db        461 NWAECFA 467


RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 467
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:consensus
;    OTHER INFORMATION: sequence
US-09-634-493A-2

  Query Match             92.2%;  Score 2270;  DB 4;  Length 467;
  Best Local Similarity   89.7%;  Pred. No. 5.5e-229;
  Matches  437;  Conservative    3;  Mismatches    7;  Indels   40;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
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Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              |||||||||||||||||||||||||||||| ||||||                   |||
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSA-------------------TYN 100

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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Db        101 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160

Qy        181 KLADPGSQPHQASPVIN-------------------VIIPEGSGYNNTLDHGTCTAFED 220
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Db        161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy        221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSP 280
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Db        221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

Qy        281 FCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
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Db        281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy        341 TLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWT 400
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Db        341 TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

Qy        401 VPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460
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Qy        461 NWAECFA 467
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Db        461 NWAECFA 467


RESULT 6
US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
```

```
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/923,724
;       FILING DATE:  31-JUL-1992
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/496,155
;       FILING DATE:  19-MAR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/044,077
;       FILING DATE:  29-APR-1987
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  UK 8610600
;       FILING DATE:  30-APR-1986
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Cimbala, Michele A.
;       REGISTRATION NUMBER:  33,851
;       REFERENCE/DOCKET NUMBER:  1050.0240004
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-07-923-724-8

  Query Match             76.3%;  Score 1879;  DB 1;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 5.1e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||  ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:|:||||:|
Db          1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ||||||||  ||||| ||||||||||||  |  | ||||| ||:| | | |||||||||
Db         61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:' | |  ||||| |||| :||||| | ||||||| |||:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
               ||| || |||||| :| |||||| |||:: ::  |:|||:| |||||||| ||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
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Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| |||||||||||||||:||:| :|||:|::|||||:| |||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
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Db        421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467
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RESULT 7
US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;     APPLICANT:  Nevalainen, Helena K.M.
;     APPLICANT:  Paloheimo, Marja T.
;     APPLICANT:  Miettinen-Oinonen, Arja S.K.
;     APPLICANT:  Torkkeli, Tuula K.
;     APPLICANT:  Cantrell, Michael
;     APPLICANT:  Piddington, Christopher S.
;     APPLICANT:  Rambosek, John A.
;     APPLICANT:  Turunen, Marja K.
;     APPLICANT:  Fagerstr m, Richard B.
;     APPLICANT:  Houston, Christine S.
;     TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;     TITLE OF INVENTION:  in Trichoderma
;     NUMBER OF SEQUENCES:  69
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;       STREET:  1100 New York Avenue, Suite 600
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  U.S.A.
;       ZIP:  20005
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/609,426A
;       FILING DATE:  01-MAR-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/923,724
;       FILING DATE:  31-JUL-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/496,155
;       FILING DATE:  19-MAR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/044,077
;       FILING DATE:  29-APR-1987
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  UK 8610600
;       FILING DATE:  30-APR-1986
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Reed, Grant E.
;       REGISTRATION NUMBER:  P-41,264
;       REFERENCE/DOCKET NUMBER:  1050.008000I
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 371-2600
;       TELEFAX:  (202) 371-2540
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-609-426A-8

  Query Match             76.3%;  Score 1879;  DB 2;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 5.1e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||  ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:|:||||:|
Db          1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ||||||||  ||||| ||||||||||||  |  | ||||| ||:| | | |||||||||
Db         61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120
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Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| |||:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
              ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNAILYADFS 360
              ||||:|||||||| ||||:|||||||||||||| | ||:|||||||||||||:|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGIKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| |||||||||||||||:||:| :|||:|::|||||:| ||||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              |||||||||||||||| :| |||| || || |||:|||||:|||| |
Db        421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT 8
US-08-374-652C-2
; Sequence 2, Application US/08374652C
; Patent No. 5834286
;  GENERAL INFORMATION:
;    APPLICANT:  NEVALAINEN, HELENA K.M.
;    APPLICANT:  PALOHEIMO, MARJA T.
;    APPLICANT:  FAGERSTROM, RICHARD B.
;    APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;    APPLICANT:  TURUNEN, MARJA K.
;    APPLICANT:  RAMBOSEK, JOHN A.
;    APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;    APPLICANT:  HOUSTON, CHRISTINE S.
;    APPLICANT:  CANTRELL, MICHAEL A.
;    TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;    TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;    TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;    NUMBER OF SEQUENCES:  94
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/374,652C
;      FILING DATE:  24-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/07058
;      FILING DATE:  27-JUL-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/925,401
;      FILING DATE:  31-JUL-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  REED, GRANT E.
;      REGISTRATION NUMBER:  41,264
;      REFERENCE/DOCKET NUMBER:  1050.071001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
US-08-374-652C-2

  Query Match            76.3%;  Score 1879;  DB 2;  Length 467;
  Best Local Similarity  75.6%;  Pred. No. 5.1e-188;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              ||| ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:|:||||:|
Db          1 MGVSAVLLPLYLLAGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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Db         61 SAISPDVPAGCRVTFAQVLSRHGARYPTESKGKKYSALIEEIQQNVTTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIIPFIRSSGSSRVIASGEKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| |||:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
              ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWIHYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| ||||:|||||||||||||| | ||:|||||||||||||:|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| |||||||||||||||:||:| :|||:|::|||||:| ||||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              |||||||||||||||| :| |||| || || |||:|||||:|||| |
Db        421 LVRVLVNDRVVPLHGCPIDALGRCTRDSFVRGLSFARSGGDWAECSA 467


RESULT 9
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/151,574
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-151-574-32

  Query Match             75.2%;  Score 1875;  DB 1;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 1.3e-187;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              ||| ||| :  | |  || |:    |  |||||| |||||  | |||||  |:|:|||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:||  ||||| ||||||||||||  |  | ||||||  ||:||| | ||||||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:||||||||||| ::|||||||:||::|  | ||||||:||| |||||  :||||||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFIALFAPAIR 240
              || || :|| |:|| |:|:| : |  ||||| |||| |||||| | |||||| | |:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNILDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
              ||| || |||||| :| |||:|| |||:: ::  |:|||| |||||||| |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:||:|||||| |||||:|||||||||||||| | ||:|||||:|||||||:|||||||
Db        301 KYYGHGAGNPLGPIQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| |||||||||||||||:||:| :|||:|:::|||||:| ||||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGGNWAECFA 467
              |||||||||||||||| || |||| || || |||||||||:||||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 10
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20

  Query Match             76.2%;  Score 1875;  DB 1;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 1.3e-187;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||  ||| :  | |  ||| |:    |  |||||| |||||  | |||||  |:|:|||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:||  ||||| ||||||||||||  |  | ||||||  ||:||| | ||||||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:||||||||||| ::|||||||:||::|  | ||||||:||| |||||  :||||||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| : |  ||||| |||| |||||| | |||||| | |:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
              ||| || |||||| :| |||:|| |||:: ::  |:|||| |||||||| |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDIKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:||:|||||| |||||:|||||||||||||| | ||:|||||:|||||||:|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| |||||||||||||||:||:| :|||:|:::|||||:| ||||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGGNWAECFA 467
              |||||||||||||||| || |||| || || |||||||||:||||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 11
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  VAN OOIJEN, ALBERT J.J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 PAGE MILL ROAD
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/693,709
;      FILING DATE:  07-AUG-1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/146,424
;      FILING DATE:  02-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20011.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-813-5600
;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Signal Sequence
;      LOCATION:  1...23
;      OTHER INFORMATION:
US-08-693-709-2

  Query Match            76.2%;  Score 1875;  DB 1;  Length 467;
  Best Local Similarity  75.6%;  Pred. No. 1.3e-187;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              ||| ||| :  | | ||| |:    |  |||||| ||||| | |;||| |:|:||||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:||  ||||| |||||||||||| |  | ||||| ||:|:| | ||||||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:||||||||||| ::||||||||:||::| | ||||||:||| ||||| :|||||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| | |  ||||| |||| |||||| | |||||||  | |:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
               ||| || |||||| :| |||||| |||:: ::  |:|||||| |||||||| |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| ||||:|||||||||||||| | ||:|||||||:|||||||:|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| ||||||||||||||:||:| :|||:|::|||||:| ||||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              |||||||||||||||| || |||| || || |||||||||:||||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 12
US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-419-448-32

  Query Match            76.2%;  Score 1875;  DB 2;  Length 467;
  Best Local Similarity  75.6%;  Pred. No. 1.3e-187;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              ||| ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|:||||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:||  ||||| |||||||||||| |  | ||||| ||:||| | ||||||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:||||||||||| ::||||||||:||::| | ||||||:||| ||||| :|||||||
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Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300

Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420

Db        361 HDNGIISILFALGLYNGTKPLSTTIVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467

Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 13
US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-819-825-3

  Query Match           76.2%;  Score 1875;  DB 2;  Length 467;
  Best Local Similarity  75.6%;  Pred. No. 1.3e-187;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60

Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120

Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180

Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300

Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420

Db        361 HDNGIISILFALGLYNGTKPLSTTIVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467

Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 14
US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,642
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-163-642-3
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  Query Match             76.2%;  Score 1875;  DB 3;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 1.3e-187;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|:||||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:||  ||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:||||||||||| ::|||||||:||::| | ||||||:||| ||||| :||||||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| | |:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
               ||| || |||||| :| ||||| |||:: ::  |:|||| |||||||| ||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| ||||:|||||||||||| | ||:|||||:|||||||:|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| ||||||||||:|||||:|||| :|:|:|::|||||:| ||||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              |||||||||||||:|| |: |||| |. || ||||||||:||:.||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 15
US-09-233-510-32
; Sequence 32, Application US/09233510
; Patent No. 6350602
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/233,510
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-233-510-32

  Query Match             76.2%;  Score 1875;  DB 4;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 1.3e-187;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSISGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:|:||||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:||  ||||| |||||||||||| |  | |||||| ||:||| | ||||||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:||||||||||| ::|||||||:||::| | ||||||:||| ||||| :||||||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNILDHGTCIAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| | |  ||||| |||| |||||| | ||||||| | |:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
               ||| || |||||| :| ||||||  |||:: ::  |:|||| |||||||, |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| ||||:|||||||||||| | ||:|||;||:||||||:|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| ||||||||||||||:||:| :|||:|::|||||:| ||||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              |||||||||||||| :| |||| || || |||||||||:|||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


Search completed: October  3, 2003, 07:47:49
Job time : 13.9581 secs
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NO

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 ; Search time 106.714 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-29
Perfect score: 2462
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWAECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2408	97.8	467	14	US-10-083-452-9	Sequence 9, Appli
2	1875	76.2	467	15	US-10-079-709-32	Sequence 32, Appl
3	1875	76.2	467	15	US-10-229-358-5	Sequence 5, Appli
4	1867	75.8	465	14	US-10-083-452-8	Sequence 8, Appli
5	1867	75.8	465	15	US-10-062-848-78	Sequence 78, Appl
6	1867	75.8	465	15	US-10-229-358-6	Sequence 6, Appli
7	1863	75.7	467	14	US-10-083-452-11	Sequence 11, Appl
8	1860.5	75.6	474	15	US-10-213-990-24	Sequence 24, Appl
9	1860	75.5	467	9	US-09-929-060-3	Sequence 3, Appli
10	1859	75.5	465	15	US-10-062-848-80	Sequence 80, Appl
11	1858	75.5	465	15	US-10-062-848-79	Sequence 79, Appl
12	1857.5	75.4	439	15	US-10-062-848-3	Sequence 3, Appli
13	1857.5	75.4	449	15	US-10-062-848-12	Sequence 12, Appl
14	1855	75.3	465	15	US-10-062-848-81	Sequence 81, Appl
15	1851	75.2	462	15	US-10-229-358-12	Sequence 12, Appl
16	1845	74.9	469	15	US-10-062-848-82	Sequence 82, Appl
17	1835.5	74.6	463	14	US-10-083-452-10	Sequence 10, Appl
18	1833	74.5	444	15	US-10-062-848-1	Sequence 1, Appli
19	1820.5	73.9	447	15	US-10-062-848-6	Sequence 6, Appli
20	1818	73.8	443	9	US-09-929-060-1	Sequence 1, Appli
21	1813	73.6	443	9	US-09-929-060-2	Sequence 2, Appli
22	1765	71.7	450	15	US-10-062-848-15	Sequence 15, Appl
23	1761	71.5	466	14	US-10-083-452-12	Sequence 12, Appl
24	1761	71.5	466	15	US-10-229-358-7	Sequence 7, Appli
25	1719	69.8	466	14	US-10-083-452-13	Sequence 13, Appl
26	1715.5	69.7	450	15	US-10-062-848-9	Sequence 9, Appli
27	1714	69.6	438	15	US-10-062-848-2	Sequence 2, Appli
28	1627	66.1	489	15	US-10-229-358-4	Sequence 4, Appli
29	1627	66.1	489	15	US-10-229-358-10	Sequence 10, Appl
30	1613	65.5	410	15	US-10-229-358-11	Sequence 11, Appl
31	1334	54.2	475	14	US-10-083-452-14	Sequence 14, Appl
32	1313.5	53.4	487	14	US-10-083-452-15	Sequence 15, Appl
33	1313.5	53.4	487	15	US-10-229-358-8	Sequence 8, Appli
34	1311	53.2	355	15	US-10-229-358-15	Sequence 15, Appl
35	1187	48.2	495	14	US-10-083-452-2	Sequence 2, Appli
36	1182	48.0	478	14	US-10-083-452-3	Sequence 3, Appli
37	902	36.6	284	15	US-10-229-358-19	Sequence 19, Appl
38	855	34.7	283	15	US-10-229-358-9	Sequence 9, Appli
39	855	34.7	283	15	US-10-229-358-24	Sequence 24, Appl
40	802.5	32.6	443	14	US-10-083-452-5	Sequence 5, Appli
41	798.5	32.4	439	14	US-10-083-452-7	Sequence 7, Appli
42	795.5	32.3	453	14	US-10-083-452-6	Sequence 6, Appli
43	781	31.7	442	14	US-10-083-452-4	Sequence 4, Appli
44	702.5	28.5	212	15	US-10-229-358-16	Sequence 16, Appl
45	401	16.3	312	15	US-10-229-358-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 97.8%; Score 2408; DB 14; Length 467;
Best Local Similarity 97.9%; Pred. No. 4.1e-230;
Matches 457; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||
Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||:||
Db        181 KLADPGSQPHQASPVIDVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
              |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        241 ARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLG 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              |||||:|||||||||||||||||||||| |||:|||||||||||||||||||||||||||||||||||
Db        301 KYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              |||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 HDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQAEKEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467


RESULT 2
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/079,709
;      FILING DATE:  02-FEB-2002
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/233,510
;      FILING DATE:  20-JAN-1999
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-079-709-32

  Query Match             76.2%;  Score 1875;  DB 15;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 3.4e-177;
  Matches  353;  Conservative   41;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||  ||| :  | | ||| |:    | |||||| |||| | ||||| |:|:|||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:|| |||| ||||||||||| |  | |||||| ||:||| | ||||||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:|||||||||||| ::|:|||||||:||::| | ||||||:||| |||| :|||||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| | |  |||| |||| |||||| | ||:|||| / |:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
               ||| || |||||| :| |||||| |||:: ::  |:||||| |||||||| |||||||
Db        241 QRLENDLSGVTLTDIEVTYLMDMCSFDTISTSIVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| ||||:|||||||||||||| | ||:|||||:|||||||:|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| |||||||||||||||:||:| :|||:|::|||||:| ||||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              |||||||||||||||| || |||| || || ||||||||||:||||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 3
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-229-358-5

  Query Match             76.2%;  Score 1875;  DB 15;  Length 467;
  Best Local Similarity   75.6%;  Pred. No. 3.4e-177;
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Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db          1 MGVSAVLLPLYLLSGVISGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNAITFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467
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RESULT 4
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

Query Match 75.8%; Score 1867; DB 14; Length 465;
Best Local Similarity 76.0%; Pred. No. 2.1e-176;
Matches 355; Conservative 36; Mismatches 74; Indels 2; Gaps 2;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db        180 KLADPGA-TNRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
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RESULT 5
US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-78

Query Match 75.8%; Score 1867; DB 15; Length 465;
Best Local Similarity 76.0%; Pred. No. 2.1e-176;
Matches 355; Conservative 36; Mismatches 74; Indels 2; Gaps 2;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179
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Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db        180 KLADPGA-TNRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPAIFPLNATMYVDFS 358

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 6
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-229-358-6

  Query Match             75.8%;  Score 1867;  DB 15;  Length 465;
  Best Local Similarity   76.0%;  Pred. No. 2.1e-176;
  Matches  355;  Conservative   36;  Mismatches   74;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db        180 KLADPGA-TNRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPAIFPLNATMYVDFS 358

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 7
US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
;  APPLICANT: Svendsen, Allan
;  TITLE OF INVENTION: Phytase Variants
;  FILE REFERENCE: 5618.500-US
;  CURRENT APPLICATION NUMBER: US/10/083,452
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: US/09/273,871
;  PRIOR FILING DATE: 1999-03-22
;  PRIOR APPLICATION NUMBER: PA 1998 00407
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: PA 1998 00806
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: PA 1998 01176
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: PA 1999 00091
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/080,129
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/090,675
;  PRIOR FILING DATE: 1998-06-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus ficuum
US-10-083-452-11

  Query Match             75.7%;  Score 1863;  DB 14;  Length 467;
  Best Local Similarity   75.2%;  Pred. No. 5.2e-176;
  Matches  351;  Conservative   41;  Mismatches   75;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLIRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db        241 QRLENDLSGVTLTDIEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLKSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQAP 420
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Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              ||||||||||||||| || |||| || || |||||||||:||||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 8
US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Bo
;  APPLICANT:  Bussey, Howard
;  APPLICANT:  Storms, Reg
;  APPLICANT:  Roemer, Terry
;  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
;  TITLE OF INVENTION:  ENZYMES AND METHODS OF USE
;  FILE REFERENCE: 10182-019-999
;  CURRENT APPLICATION NUMBER: US/10/213,990
;  CURRENT FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Aspergillus
US-10-213-990-24

  Query Match             75.6%;  Score 1860.5;  DB 15;  Length 474;
  Best Local Similarity   75.3%;  Pred. No. 9.5e-176;
  Matches  351;  Conservative   41;  Mismatches   67;  Indels    7;  Gaps    2;

Qy          2 GVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADES 61
              |  |::|  : :  : |          | |||||| |||| |  |||| |||:||| ||
Db         16 GAVVLILKRSRVSAAPSS------AGSKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDEL 69

Qy         62 AISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNY 121
              :::  :| |||:| ||||||||||||||| || |  |: ||| ||| ||||:||||||||
Db         70 SVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNY 129

Qy        122 TLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSAK 181
              |||||||||||| |:||||||||:||||||| :|||||||||:|||| |||||||| ||
Db        130 TLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQAK 189

Qy        182 LADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRA 241
              | |||:  ::|:| |:|||||   :|||||||| || || |:|||:| |||||||| ||
Db        190 LADPGA-TNRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIRA 248

Qy        242 RLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLGK 301
              | |  |||||||||:||| |||||| ||||||||||::|||:| ||||:|| :|:||||:|
Db        249 RAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGK 308

Qy        302 YYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNAILYADFSH 361
              ||||||||||||||:|| |||||||| |||||||||| || |||||:||||:| ||||
Db        309 YYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHITSTNSTLVSNPATFPLNATMYVDFSH 368

Qy        362 DNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEPL 421
              ||:|:|||||||||||:||| ||||| :| ||||||| ||| |||| | ||||:|||||
Db        369 DNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEPL 428

Qy        422 VRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              || |:|||||||:|| |||||||| :|||:|||:|||||:| |||:
Db        429 VRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 474


RESULT 9
US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
;  APPLICANT: KONDO, HIDEMASA
;  APPLICANT:  ANAZAWA, HIDEHARU
;  APPLICANT:  KANEKO, SYUNICHI
;  APPLICANT:  NAGASHIMA, TADASHI
;  APPLICANT:  IANGE, TATSUYA
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 081356/0166
;  CURRENT APPLICATION NUMBER: US/09/929,060
;  CURRENT FILING DATE:  2001-08-05
;  PRIOR APPLICATION NUMBER: 09/543,744
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: 09/155,855
;  PRIOR FILING DATE: 1998-10-05
;  PRIOR APPLICATION NUMBER: JP 084314/1996
;  PRIOR FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 467
; ' TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-929-060-3

  Query Match             75.5%;  Score 1860;  DB 9;  Length 467;
  Best Local Similarity   74.1%;  Pred. No. 1e-175;
  Matches  346;  Conservative   48;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||  ||| :  | | ||| |:    |  :||||| ||||| | ||||| |:|:||||::
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANK 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ||||||||  | ||| |||||||||||| |  | |||||| ||:||| |:|||||||||
Db         61 SAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFEGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:|||||||||| ::||||:|||:||::| | |||||||||| |||||  ||||||||
Db        121 YSLGADDLTPFGEQELVNSGVKFYQRYESLTRNIVPFIRSSGSSRVIASGNKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| | |  ||||| |||| |||||| ||:|||||| | |:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASTSNNTLDPGTCTVFEDSELADDIEANFTATFVPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
              ||| || ;|:||| :| |||||| |||:: ::  |:||||| ||||:||| ||||||;
Db        241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSIVDTKLSPFCDLFTHEEWINYDYLQSLN 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              |||:|||||||| ||||:|||||||||||| | ||:|||||||'||||||:|||||||
Db        301 KYYGHGAGNPLGPIQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| |||||||||||||:|: |:| :|||:|::|||||:: |||||||||:|:||
Db        361 HDNGIISILFALGLYNGTKPLSSTTAENITQTDGFSSAWTVPFASRMYVEMMQCQSEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              |||||||||:|||| || |||| || ||:|||||||||:| ||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVKGLSFARSGGDWGECFA 467


RESULT 10
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
```

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;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-80

  Query Match            75.5%;  Score 1859;  DB 15;  Length 465;
  Best Local Similarity  75.8%;  Pred. No. 1.3e-175;
  Matches  354;  Conservative   36;  Mismatches   75;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  ||||| |||:||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
               ::|  :| |||:| ||||||||||||||| || |  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||| |:||:|||||:||||||| :|||||||||||||||| |||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              :||||||:  ::|:| |:|.||| :|||||||| || ||  |:|.|:| |||||||||  ||
Db        180 KLADPGA-TNRAAPAISVIIPESETFNNTLDHGVCIKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
              || |  |||||||||||| ||||| ||||||||||::|||| |||:|| :|:||||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              |||:|:|||||||||||:||| ||||| :| ||||||| ||| |||| | ||||::|||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFEIMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:|||||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 11
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-79

  Query Match            75.5%;  Score 1858;  DB 15;  Length 465;
  Best Local Similarity  75.8%;  Pred. No. 1.6e-175;
  Matches  354;  Conservative   36;  Mismatches   75;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  ||||| |||:||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
               ::|  :| |||:| ||||||||||||||| || |  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||| |:||:|||||:||||||| :|||||||||||||||| |||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              :||||||:  ::|:| |:|.||| :|||||||| || ||  |:|.|:| |||||||||  ||
Db        180 KLADPGA-TNRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
              || |  |||||||||||| ||||| ||||||||||::|||| |||:|| :|:||||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              |||:|:|||||||||||:||| ||||| :| ||||||| ||| |||| | ||||::|||
Db        359 HDNSMVSIFFALGLYNGTEGLSRTSVESAKELDGYSASWVVPFGARAYFEIMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:|||||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 12
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-3

  Query Match            75.4%;  Score 1857.5;  DB 15;  Length 439;
  Best Local Similarity  78.9%;  Pred. No. 1.7e-175;
  Matches  347;  Conservative   36;  Mismatches   56;  Indels    1;  Gaps    1;

Qy         28 SHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARYP 87
              | |||||| |||| |  ||||| |||:||| || ::|  :| |||:| ||||||||||||
Db          1 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 60
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Qy         88 TSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLIPFGENQMVNSGIKFYRRY 147
Db         61 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLIPFGEQQLVNSGIKFYQRY 120

Qy        148 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGYN 207
Db        121 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGA-TNRAAPAISVIIPESETFN 179

Qy        208 NTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFD 267
Db        180 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFD 239

Qy        268 TVARTSDAIELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARL 327
Db        240 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 299

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVE 387
Db        300 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 359

Qy        388 SIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRD 447
Db        360 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 419

Qy        448 DFVEGLSFARSGGNWAECFA 467
Db        420 DFVKGLSWARSGGNWGECFS 439


RESULT 13
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-12

  Query Match           75.4%;  Score 1857.5;  DB 15;  Length 449;
  Best Local Similarity  78.9%;  Pred. No. 1.7e-175;
  Matches  347;  Conservative   36;  Mismatches   56;  Indels    1;  Gaps    1;

Qy         28 SHSCDTVDGGYQCFPEISHLWGTYSPYFSLADESAISPDVPDDCRVTFVQVLSRHGARYP 87
Db         11 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 70

Qy         88 TSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 147
Db         71 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 130

Qy        148 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVINVIIPEGSGYN 207
Db        131 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGA-TNRAAPAISVIIPESETFN 189

Qy        208 NTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFD 267
Db        190 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFD 249

Qy        268 TVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARL 327
Db        250 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 309

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVE 387
Db        310 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 369

Qy        388 SIEETDGYSASWTVPFAARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRD 447
Db        370 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 429

Qy        448 DFVEGLSFARSGGNWAECFA 467
Db        430 DFVKGLSWARSGGNWGECFS 449


RESULT 14
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-81

  Query Match           75.3%;  Score 1855;  DB 15;  Length 465;
  Best Local Similarity  75.6%;  Pred. No. 3.2e-175;
  Matches  353;  Conservative   37;  Mismatches   75;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTAFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db        180 KLADPGA-TNRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
Db        239 ARAKKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
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Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              |||:|:|||||||||||||:||| ||||| :| |.|||| ||| |||| | |||::||||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:||||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 15
US-10-229-358-12
; Sequence 12, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-229-358-12

  Query Match             75.2%;  Score 1851;  DB 15;  Length 462;
  Best Local Similarity   75.5%;  Pred. No. 8e-175;
  Matches  349;  Conservative   41;  Mismatches   72;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPYFSLADE 60
              |||  ||| :  | | ||| ||:    |  |||||| ||||| | ||||| |:|:||||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:||  ||||| ||:|||||||||| |  | |||||| ||:||| | ||||||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:|||||||||'|| ::|:|||||||:||::| | ||||||:||| |||| :|||||,|
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGSQPHQASPVINVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
              || || :|| |:|| |:|:| | |  |||| |||| |||||| | |||||| |||:||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFAPSIR 240

Qy        241 ARLEADLPGVTLTDEDVVYLMDMCPFDTVARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
               ||| || |||||| :| |||||| |||:: ::  |:|||| |||||||| |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| ||||:|||||||||||||| | ||:|||||:|||||||:|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCQAEKEP 420
              ||| :||| ||||||||||||||||:||:| :|||:|::|||||:| |||||||||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNW 462
              |||||||||||||||| || |||| || || ||||||||:|
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDW 462


Search completed: October  3, 2003, 08:12:30
Job time : 107.714 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 ; Search time 106.714 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-31
Perfect score: 2468
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWEECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2308	93.5	467	14	US-10-083-452-9	Sequence 9, Appli
2	1888	76.5	465	14	US-10-083-452-8	Sequence 8, Appli
3	1888	76.5	465	15	US-10-062-848-78	Sequence 78, Appl
4	1888	76.5	465	15	US-10-229-358-6	Sequence 6, Appli
5	1881.5	76.2	474	15	US-10-213-990-24	Sequence 24, Appl
6	1880	76.2	465	15	US-10-062-848-80	Sequence 80, Appl
7	1879	76.1	465	15	US-10-062-848-79	Sequence 79, Appl
8	1878.5	76.1	439	15	US-10-062-848-3	Sequence 3, Appli
9	1878.5	76.1	449	15	US-10-062-848-12	Sequence 12, Appl
10	1876	76.0	465	15	US-10-062-848-81	Sequence 81, Appl
11	1854	75.1	469	15	US-10-062-848-82	Sequence 82, Appl
12	1848	74.9	467	15	US-10-079-709-32	Sequence 32, Appl
13	1848	74.9	467	15	US-10-229-358-5	Sequence 5, Appli
14	1841	74.6	467	9	US-09-929-060-3	Sequence 3, Appli
15	1836	74.4	467	14	US-10-083-452-11	Sequence 11, Appl
16	1829	74.1	462	15	US-10-229-358-12	Sequence 12, Appl
17	1806	73.2	444	15	US-10-062-848-1	Sequence 1, Appli
18	1804.5	73.1	463	14	US-10-083-452-10	Sequence 10, Appl
19	1799	72.9	443	9	US-09-929-060-1	Sequence 1, Appli
20	1794	72.7	443	9	US-09-929-060-2	Sequence 2, Appli
21	1789.5	72.5	447	15	US-10-062-848-6	Sequence 6, Appli
22	1752	71.0	466	14	US-10-083-452-12	Sequence 12, Appl
23	1752	71.0	466	15	US-10-229-358-7	Sequence 7, Appli
24	1748	70.8	450	15	US-10-062-848-15	Sequence 15, Appl
25	1710	69.3	466	14	US-10-083-452-13	Sequence 13, Appl
26	1706.5	69.1	450	15	US-10-062-848-9	Sequence 9, Appli
27	1697	68.8	438	15	US-10-062-848-2	Sequence 2, Appli
28	1658	67.2	489	15	US-10-229-358-4	Sequence 4, Appli
29	1658	67.2	489	15	US-10-229-358-10	Sequence 10, Appl
30	1623	65.8	410	15	US-10-229-358-11	Sequence 11, Appl
31	1381	56.0	475	14	US-10-083-452-14	Sequence 14, Appl
32	1339	54.3	355	15	US-10-229-358-15	Sequence 15, Appl
33	1334.5	54.1	487	14	US-10-083-452-15	Sequence 15, Appl
34	1334.5	54.1	487	15	US-10-229-358-8	Sequence 8, Appli
35	1215	49.2	495	14	US-10-083-452-2	Sequence 2, Appli
36	1210	49.0	478	14	US-10-083-452-3	Sequence 3, Appli
37	920	37.3	284	15	US-10-229-358-19	Sequence 19, Appl
38	867	35.1	283	15	US-10-229-358-9	Sequence 9, Appli
39	867	35.1	283	15	US-10-229-358-24	Sequence 24, Appl
40	845.5	34.3	443	14	US-10-083-452-5	Sequence 5, Appli
41	833.5	33.8	453	14	US-10-083-452-6	Sequence 6, Appli
42	830.5	33.7	439	14	US-10-083-452-7	Sequence 7, Appli
43	825	33.4	442	14	US-10-083-452-4	Sequence 4, Appli
44	729.5	29.6	212	15	US-10-229-358-16	Sequence 16, Appl
45	406	16.5	312	15	US-10-229-358-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 93.5%; Score 2308; DB 14; Length 467;
Best Local Similarity 93.4%; Pred. No. 6.9e-224;
Matches 436; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
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Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ||||||| ||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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Db        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 KLADPGSQPHQASPVIDVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              ||||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLG 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHISTNHILDSNPATFPLNATLYADFS 360
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        301 KYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNHILDSNPATFPLNATLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|:|||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        361 HDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQAEKEP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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Db        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
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RESULT 2
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

Query Match 76.5%; Score 1888; DB 14; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.6e-181;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

```
Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | ||||||| |||| |  ||||| |||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59
```

```
Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ::|  :|| ||:| ||||||||||||||| || |  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              ||||||||||||||||:|||||||:|||||||  :|||||||||||||| |||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :|||||||:|| || |:|||:| |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||'|| |||||||:||||| ||||||||||:|||||| ||||:|, :|:||||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHISTNHILDSNPATFPLNATLYADFS 360
              ||||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSILVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||:||| |||||  :| ||||||| ||| |||| | |||::||||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||.| |||||||| :|||:|||:|||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
```

RESULT 3
US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-78

Query Match 76.5%; Score 1888; DB 15; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.6e-181;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

```
Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | ||||||| |||| |  ||||| |||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ::|  :|| ||:| ||||||||||||||| || |  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              ||||||||||||||||:|||||||:|||||||  :|||||||||||||| |||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 4
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-229-358-6

  Query Match             76.5%;  Score 1888;  DB 15;  Length 465;
  Best Local Similarity   76.9%;  Pred. No. 1.6e-181;
  Matches  359;  Conservative   35;  Mismatches   71;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 5
US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Bo
;  APPLICANT:  Bussey, Howard
;  APPLICANT:  Storms, Reg
;  APPLICANT:  Roemer, Terry
;  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
;  TITLE OF INVENTION:  ENZYMES AND METHODS OF USE
;  FILE REFERENCE: 10182-019-999
;  CURRENT APPLICATION NUMBER: US/10/213,990
;  CURRENT FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Aspergillus
US-10-213-990-24

  Query Match             76.2%;  Score 1881.5;  DB 15;  Length 474;
  Best Local Similarity   76.2%;  Pred. No. 7.7e-181;
  Matches  355;  Conservative   40;  Mismatches   64;  Indels    7;  Gaps    2;

Qy          2 GVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADES 61
Db         16 GAVVLILKRSRVSAAPSS------AGSKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDEL 69

Qy         62 AISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNY 121
Db         70 SVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNY 129

Qy        122 TLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSAK 181
Db        130 TLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQAK 189

Qy        182 LADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241
Db        190 LADPGAT-NRAAPAISVIIPESETFNNILDHGVCTKFEASQLGDEVAANFTALFAPDIRA 248

Qy        242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK 301
Db        249 RAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGK 308

Qy        302 YYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSH 361
Db        309 YYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSH 368

Qy        362 DNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPL 421
Db        369 DNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEPL 428

Qy        422 VRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        429 VRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 474


RESULT 6
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSIREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
```

```
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-80

  Query Match             76.2%;  Score 1880;  DB 15;  Length 465;
  Best Local Similarity   76.7%;  Pred. No. 1.1e-180;
  Matches  358;  Conservative   35;  Mismatches   72;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDIVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  |||| |||||||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                ::|  :|| ||:| ||||||||:|||||| || |  |: ||| ||| ||||:|||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:|||||||:|||||| :|||||||||||||| ||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              ||||||| ::|:| |:|||||   :||||||:|| || |:|||:| |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNILDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:||||| |||||||||:|||||| ||||:|| :|:||||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              |||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| ||||| :| ||||||| ||| |||| | |||::|||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKES 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:|||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 7
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-79

  Query Match             76.1%;  Score 1879;  DB 15;  Length 465;
  Best Local Similarity   76.7%;  Pred. No. 1.3e-180;
  Matches  358;  Conservative   35;  Mismatches   72;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  |||| |||||||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                ::|  :|| ||:| ||||||||:|||||| || |  |: ||| ||| ||||:|||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:|||||||:|||||| :|||||||||||||| ||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              ||||||| ::|:| |:|||||   :||||||:|| || |:|||:| |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNILDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:||||| |||||||||:|||||| ||||:|| :|:||||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              |||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGIKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:|| ||||| :| ||||||| ||| |||| | |||::|||
Db        359 HDNSMVSIFFALGLYNGTEGLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:|||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 8
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
```

US-10-062-848-3

Query Match 76.1%; Score 1878.5; DB 15; Length 439;
Best Local Similarity 79.8%; Pred. No. 1.4e-180;
Matches 351; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

```
Qy         28 SHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 87
              | |||||| |||| |  |.||| ||||||| || ::|  :|| ||:| |||||||||||
Db          1 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 60

Qy         88 TSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRY 147
              ||| || |  |: ||| ||| |||||:|||||||||||||||||||||||:|||||||:|:|
Db         61 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 120

Qy        148 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYN 207
              ||||| :|||||||||||||| |||||||| ||||||||  ::|:| |:|||||   :|
Db        121 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGAT-NRAAPAISVIIPESETFN 179

Qy        208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFD 267
              ||||||:|| || |:||||:| ||||||:||| |||| | ||||| |||||||:||||| ||
Db        180 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLIDEDVVSLMDMCSFD 239

Qy        268 TVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
              |||||||||:|||||| ||||:|| :|:|||||||||||||||||:||| |||||||||
Db        240 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 299

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE 387
              | |||||||||| || |||:|||||||:| ||||||:|||||||||||||:||| ||||
Db        300 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 359

Qy        388 SIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
              | :| ||||||| ||| |||| | |||::|||||||| |:|||||||||| ||||||| :
Db        360 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 419

Qy        448 DFVEGLSFARSGGNWEECFA 467
              |||:|||:||||||| |||:
Db        420 DFVKGLSWARSGGNWGECFS 439
```

RESULT 9
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSIREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 76.1%; Score 1878.5; DB 15; Length 449;
Best Local Similarity 79.8%; Pred. No. 1.4e-180;
Matches 351; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

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Qy         28 SHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 87
              | |||||| |||| |  |.||| ||||||| || ::|  :|| ||:| |||||||||||
Db         11 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 70

Qy         88 TSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRY 147
              ||| || |  |: ||| ||| |||||:|||||||||||||||||||||||:|||||||:|:|
Db         71 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 130

Qy        148 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYN 207
              ||||| :|||||||||||||| |||||||| ||.|||||  ::|:| |:|||||   :|
Db        131 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGAT-NRAAPAISVIIPESETFN 189

Qy        208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFD 267
              ||||||:|| || |:||||:| ||||||:||| |||| | ||||| |||||||:||||| ||
Db        190 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFD 249

Qy        268 TVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
              |||||||||:|||||| ||||:|| :|:|||||||||||||||||:||| |||||||||
Db        250 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 309

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE 387
              | |||||||||| || |||:|||||||:| ||||||:|||||||||||||:||| ||||
Db        310 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 369

Qy        388 SIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
              | :| ||||||| ||| |||| | |||::|||||||| |:|||||||||| ||||||| :
Db        370 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 429

Qy        448 DFVEGLSFARSGGNWEECFA 467
              |||:|||:||||||| |||:
Db        430 DFVKGLSWARSGGNWGECFS 449
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RESULT 10
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSIREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 76.0%; Score 1876; DB 15; Length 465;
Best Local Similarity 76.4%; Pred. No. 2.7e-180;
Matches 357; Conservative 36; Mismatches 72; Indels 2; Gaps 2;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  |||| |||||||  ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
                ::|  :|| ||:| |||||||||||||||| || |  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              ||||||||| |||||:|||||||:|||||| :|||||||||||||| |||||||| |
Db        120 YTLGADDLTAFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179
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Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :|||||||:|| || |:|||:| |||||:||| |:
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || : ||||| |||||||:|||| |||||||||:|||||| ||||:|| ::|||||
Db        239 ARAKKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              |||||||||||||||:|| |||||||| |||||||||: || ||||||||||:. |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| |||||  :| |||||||  ||| |||| | ||||:|||!
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |:|||||| :|||:|||:|||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 11
US-10-062-848-82
; Sequence 82, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 469
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-82

  Query Match             75.1%;  Score 1854;  DB 15;  Length 469;
  Best Local Similarity   73.8%;  Pred. No. 4.5e-178;
  Matches  347;  Conservative   50;  Mismatches   69;  Indels    4;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSG---TALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSL 57
              ||    |||:  |    :|   :       | :||||: |||| |  |||:| |||||
Db          1 MGALTFLLSVMYLLSGVAGAPSSGCSAGSGSKACDTVELGYQCSPGTSHLWGQYSPFFSL 60

Qy         58 ADESAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLK 117
              || ::! |:|| |||||||||||||||||:| || |  |: |||||| ||||:|||:
Db         61 EDELSVSSDLPKDCRVTFVQVLSRHGARYPTASKSKKYKKLVTAIQKNATEFKGKFAFLE 120

Qy        118 TYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGF 177
              |||||||||||||||||||||||||||::|||||  :|||||:|||||||||| ||||||
Db        121 TYNYTLGADDLTPFGEQQMVNSGIKFYQKYKALAGSVVPFIRSSGSDRVIASGEKFIEGF 180

Qy        178 QSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAP 237
              | | :|||||  ::|:|||:|||||   |||||| :|| || ||||||:|||||:|||
Db        181 QQANVADPGAT-NRAAPVISVIIPESETYNNTLDHSVCTNFEASELGDEVEANFTALFAP 239

Qy        238 PIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQ 297
              ||||:| ||||| |||:|||:|||||  ||'|||||:|||:|||||  :|||:|| :|||||
Db        240 AIRARIEKHLPGVQLTDDDVVSLMDMCSFDTVARTADASELSPFCAIFTHNEWKKYDYLQ 299

Qy        298 SLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYA 357
              \       -
              |||||||||||||||||||:|| |||||||:|||||||| |||:|||||||||||;:|
Db        300 SLGKYYGYGAGNPLGPAQGIGFTNELIARLTNSPVQDHTSTNSILDSDPATFPLNATIYV 359

Qy        358 DFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAE 417
              |||||| |: ||||:|||||:||| || || :|::|||||| ||| |||| | |||::|
Db        360 DFSHDNGMIPIFFAMGLYNGTEPLSQTSEESTKESNGYSASWAVPFGARAYFETMQCKSE 419

Qy        418 KEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              |||||| |:|||||||||| |||||||  |||:|||:|||||| |: |:
Db        420 KEPLVRALINDRVVPLHGCAVDKLGRCKLKDFVKGLSWARSGGNSEQSFS 469


RESULT 12
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/079,709
;      FILING DATE:  02-FEB-2002
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/233,510
;      FILING DATE:  20-JAN-1999
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-079-709-32

  Query Match             74.9%;  Score 1848;  DB 15;  Length 467;
  Best Local Similarity   74.3%;  Pred. No. 1.8e-177;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |||  ||| :  | | ||| |:    |  |||||| ||||| | ||||| |:||||||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:|| |||||| |||||||||||| |  | |||||| ||:|:|| | ||||||||||
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Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:|||||.|.|||:..|||||||:||::: | |||||: || |||| :|.|||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              || || | | |:|| |:|:| | :  ||||| | || ||:||| | |||||||| | | ||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
               |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||: |||'|||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| |||||: |||||||||||| | ||:|||||:|||||||:|||||::
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              ||| ::|| |||||||||||||||||:||:| :|||:|::|||||||:| |||||||:||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              |||||||||||||||| || |||| || || ||||||||||:| ||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 13
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-229-358-5

  Query Match            74.9%;  Score 1848;  DB 15;  Length 467;
  Best Local Similarity  74.3%;  Pred. No. 1.8e-177;
  Matches  347;  Conservative   42;  Mismatches   78;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDIVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |||  ||| :  | ; ||| ||:    :  |||||| |||:| | |:||| |:||| ||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:|| |||||| |||||||||:||| |  | |||||| ||:||| | |||||  |||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:|||||||||||::|||||||:||::| | ||||||:||| |||||  :|||:|||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              || || | | |:|| |:|:| | :  ||||| | || ||:||| | |||||||| | | ||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
               |||  | || ||| :|  ||||| |||:: ::  |:|||||||||||||: |||'|||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| |||||: |||||||||||| | ||:|||||:|||||||:|||||::
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              ||| ::|| |||||||||||||||||:||:| :|||:|::|||||||:| |||||||:||:||
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              |||||||||||||||| || |||| || || ||||||||||:| ||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 14
US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
;  APPLICANT: KONDO, HIDEMASA
;  APPLICANT:  ANAZAWA, HIDEHARU
;  APPLICANT:  KANEKO, SYUNICHI
;  APPLICANT:  NAGASHIMA, TADASHI
;  APPLICANT:  TANGE, TATSUYA
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 081356/0166
;  CURRENT APPLICATION NUMBER: US/09/929,060
;  CURRENT FILING DATE:  2001-08-05
;  PRIOR APPLICATION NUMBER: 09/543,744
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: 09/155,855
;  PRIOR FILING DATE: 1998-10-05
;  PRIOR APPLICATION NUMBER: JP 084314/1996
;  PRIOR FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-929-060-3

  Query Match            74.6%;  Score 1841;  DB 9;  Length 467;
  Best Local Similarity  73.2%;  Pred. No. 9.1e-177;
  Matches  342;  Conservative   49;  Mismatches   76;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |||  |||  :  | ' ||| ::    |  :||||| ||||| | |:||| |:||||||::
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANK 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              |||||:|| || ||| |||||||||||| |  | |||||| ||:||| |:||||:|||||
Db         61 SAISPDVPAGCHVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFEGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:|||||||||||::|||||:|||:|||::| | |||||:||| |||||  :|||||||
Db        121 YSLGADDLTPFGEQELVNSGVKFYQRYESLTRNIVPFIRSSGSSRVIASGNKFIEGFQST 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              || || | | |:|| |:|:| | :  ||||| | || ||:||| | |||||||| | | ||
Db        181 KLKDPRAQPGQSSPKIDVVISEASTSNNTLDPGTCTVFEDSELADDIEANFTATFVPSIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
               |||  | ||:||| :|  ||||| |||:: ::  |:|||||||||:||| |||||||
Db        241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHEEWINYDYLQSLN 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| |||||: |||||||||||| | ||:|||||:|||||||:|||||::
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              ||| ::|| |||||||||||||||:|: :|| :|||:|::|||||||:| |||||||::|:||
Db        361 HDNGIISILFALGLYNGTKPLSSTTAENITQTDGFSSAWTVPFASRMYVEMMQCQSEQEP 420
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Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||||||||||||||| || |||| || ||:|||||||||:| ||||
Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVKGLSFARSGGDWGECFA 467


RESULT 15
US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
;  APPLICANT: Svendsen, Allan
;  TITLE OF INVENTION: Phytase Variants
;  FILE REFERENCE: 5618.500-US
;  CURRENT APPLICATION NUMBER: US/10/083,452
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: US/09/273,871
;  PRIOR FILING DATE: 1999-03-22
;  PRIOR APPLICATION NUMBER: PA 1998 00407
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: PA 1998 00806
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: PA 1998 01176
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: PA 1999 00091
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/080,129
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/090,675
;  PRIOR FILING DATE: 1998-06-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus ficuum
US-10-083-452-11

  Query Match             74.4%;  Score 1836;  DB 14;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 2.9e-176;
  Matches  345;  Conservative   42;  Mismatches   80;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
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Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
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Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |:|||||||||||::|||||||:||:::| | ||||||:|||  |||||  :|||||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              ||  ||  |  |  |:|| |:|:| | :  |||||  | ||  ||:||| | |||||||  |  | ||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
               |||   |  ||  |||  :|  |||||  ||||::  ::  |:|||||||||||||| |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
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Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLKSTLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
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Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQAP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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Job time : 108.714 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.9581 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-31
Perfect score: 2468
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWEECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2308	93.5	467	4	US-09-273-871A-9	Sequence 9, Appli
2	2182	88.4	441	3	US-09-121-425-1	Sequence 1, Appli
3	2182	88.4	441	4	US-09-634-493A-1	Sequence 1, Appli
4	2170	87.9	467	3	US-09-121-425-2	Sequence 2, Appli
5	2170	87.9	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1888	76.5	465	3	US-08-868-435-33	Sequence 33, Appl
7	1888	76.5	465	4	US-08-744-231-33	Sequence 33, Appl
8	1888	76.5	465	4	US-09-044-718-78	Sequence 78, Appl
9	1888	76.5	465	4	US-09-636-499-6	Sequence 6, Appli
10	1888	76.5	465	4	US-09-273-871A-8	Sequence 8, Appli
11	1880	76.2	465	4	US-09-044-718-80	Sequence 80, Appl
12	1879	76.1	465	4	US-09-044-718-79	Sequence 79, Appl
13	1878.5	76.1	439	4	US-09-044-718-3	Sequence 3, Appli
14	1878.5	76.1	449	4	US-09-044-718-12	Sequence 12, Appl
15	1876	76.0	465	4	US-09-044-718-81	Sequence 81, Appl
16	1854	75.1	469	4	US-09-044-718-82	Sequence 82, Appl
17	1852	75.0	467	1	US-07-923-724-8	Sequence 8, Appli
18	1852	75.0	467	2	US-08-609-426A-8	Sequence 8, Appli
19	1852	75.0	467	2	US-08-374-652C-2	Sequence 2, Appli
20	1848	74.9	467	1	US-08-151-574-32	Sequence 32, Appl
21	1848	74.9	467	1	US-08-146-424-20	Sequence 20, Appl
22	1848	74.9	467	1	US-08-693-709-2	Sequence 2, Appli
23	1848	74.9	467	2	US-08-419-448-32	Sequence 32, Appl
24	1848	74.9	467	2	US-08-819-825-3	Sequence 3, Appli
25	1848	74.9	467	3	US-09-163-642-3	Sequence 3, Appli
26	1848	74.9	467	4	US-09-233-510-32	Sequence 32, Appl
27	1848	74.9	467	4	US-09-636-499-5	Sequence 5, Appli
28	1841	74.6	467	3	US-09-155-855-3	Sequence 3, Appli
29	1841	74.6	467	4	US-09-543-744-3	Sequence 3, Appli
30	1841	74.6	467	4	US-09-929-060-3	Sequence 3, Appli
31	1836	74.4	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1829	74.1	462	4	US-09-636-499-12	Sequence 12, Appl
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34	1822	73.8	466	4	US-08-744-231-35	Sequence 35, Appl
35	1819	73.7	466	3	US-08-868-435-12	Sequence 12, Appl
36	1819	73.7	466	4	US-08-744-231-12	Sequence 12, Appl
37	1806	73.2	444	4	US-09-044-718-1	Sequence 1, Appli
38	1804.5	73.1	463	3	US-08-868-435-29	Sequence 29, Appl
39	1804.5	73.1	463	4	US-08-744-231-29	Sequence 29, Appl
40	1804.5	73.1	463	4	US-09-273-871A-10	Sequence 10, Appl
41	1799	72.9	443	3	US-09-155-855-1	Sequence 1, Appli
42	1799	72.9	443	4	US-09-543-744-1	Sequence 1, Appli
43	1799	72.9	443	4	US-09-929-060-1	Sequence 1, Appli
44	1794	72.7	443	3	US-09-155-855-2	Sequence 2, Appli
45	1794	72.7	443	4	US-09-543-744-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Query Match 93.5%; Score 2308; DB 4; Length 467;
Best Local Similarity 93.4%; Pred. No. 1.2e-229;
Matches 436; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

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Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              |||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||| ||||||||||||||||||||||||:||||||||||||||||||||
Db        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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Db        181 KLADPGSQPHQASPVIDVIIPEGSGYNNTLDHGTCIAFEDSELGDDVEANFTALFAPAIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              ||||| |||| ||||||| |||||||:||||||||:|||| ||||||| ||||||||
Db        241 ARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLG 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
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Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
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Db        361 HDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQAEKEP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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Db        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467


RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

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  Matches  410;  Conservative   11;  Mismatches   20;  Indels    0;  Gaps    0;

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Qy         87 PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
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Db         61 PTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

Qy        147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY 206
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Db        121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy        207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
              ||||||| ||||||||||||||||:||| ||||||| |||| ||||||| |||||||
Db        181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

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              :|||||||||:||||| ||||||| |||||||||||||||||||||||||||||||||||
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Qy        327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
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              |||||||||||||||| |||||||||:|||||||||||||||||| |||||||||
Db        361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy        447 DDFVEGLSFARSGGNWEECFA 467
              |||||||||||||||| ||||
Db        421 DDFVEGLSFARSGGNWAECFA 441


RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-1

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  Best Local Similarity   93.0%;  Pred. No. 1.1e-216;
  Matches  410;  Conservative   11;  Mismatches   20;  Indels    0;  Gaps    0;

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Qy         87 PTSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
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Qy        147 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY 206
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Db        121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy        207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
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Db        181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

Qy        267 DTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
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Db        301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy        387 ESIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
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Db        361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy        447 DDFVEGLSFARSGGNWEECFA 467
              |||||||||||||||| ||||
Db        421 DDFVEGLSFARSGGNWAECFA 441


RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
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;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 467
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:consensus
;    OTHER INFORMATION: sequence
US-09-121-425-2

  Query Match             87.9%;  Score 2170;  DB 3;  Length 467;
  Best Local Similarity   85.4%;  Pred. No. 2.2e-215;
  Matches  416;  Conservative   11;  Mismatches   20;  Indels   40;  Gaps    2;

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Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

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Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
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Qy        181 KLADPGANPHQASPVIN------------------VIIPEGAGYNNTLDHGLCTAFEE 220
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Db        161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy        221 SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSP 280
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Db        221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

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              || ||||||| |||||||||||||||||||||||||||| |||||||| ||||||||||
Db        281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy        341 TLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWT 400
              |||||||||||||:|||||||:|:|||||||||||| |||||||||||||||||||||||
Db        341 TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

Qy        401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGG 460
              ||| |||||||:|:|||||||||||||||||||| |||||||||||||||||||||||||
Db        401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460

Qy        461 NWEECFA 467
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Db        461 NWAECFA 467


RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 467
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:consensus
;    OTHER INFORMATION: sequence
US-09-634-493A-2

  Query Match             87.9%;  Score 2170;  DB 4;  Length 467;
  Best Local Similarity   85.4%;  Pred. No. 2.2e-215;
  Matches  416;  Conservative   11;  Mismatches   20;  Indels   40;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||:||| ||
Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ||||||||  ||||||||||||||||||||| ||||||                     |||
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSA------------------TYN 100

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        101 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160

Qy        181 KLADPGANPHQASPVIN------------------VIIPEGAGYNNTLDHGLCTAFEE 220
              |||||| |||||||||:                  ||||||:||||||||| |||||:
Db        161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy        221 SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSP 280
              |||||||||||||:||| ||||||| |||| ||||||| |||||||:||||||||||:|||
Db        221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

Qy        281 FCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNH 340
              || ||||||| |||||||||||||||||||||||||||| |||||||| ||||||||||
Db        281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy        341 TLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWT 400
              |||||||||||||:|||||||:|:|||||||||||| |||||||||||||||||||||||
Db        341 TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

Qy        401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGG 460
              ||| |||||||:|:|||||||||||||||||||| |||||||||||||||||||||||||
Db        401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460

Qy        461 NWEECFA 467
              || ||||
Db        461 NWAECFA 467


RESULT 6
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33

  Query Match             76.5%;  Score 1888;  DB 3;  Length 465;
  Best Local Similarity   76.9%;  Pred. No. 2.9e-186;
  Matches  359;  Conservative   35;  Mismatches   71;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  ||||| ||||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPAISHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
               ::|  :|| ||:| |||||||||||||||| || |  |: ||| ||| ||||:|||:||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:|||||||:|||||| :|||||||||||||| |||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :|||||||:|| || |:|||:| ||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:|||||| ||||||||||:|||||| ||||:|| :|:||||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHISTNHTLDSNPATFPLNATLYADFS 360
              |||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| |||||  :| ||||:||| ||| |||| : ||||||||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:||||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 7
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
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;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33

  Query Match           76.5%;  Score 1888;  DB 4;  Length 465;
  Best Local Similarity  76.9%;  Pred. No. 2.9e-186;
  Matches  359;  Conservative   35;  Mismatches   71;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | |||:|| |||| |  |||:| |:|||: ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              :::  :|| ||:| |||:|||||||||| || |  :: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||:|||||||||||:|||||||:|||||| :|||.|||||||||| ||||:|||
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||  :|||||||:|| || |:|||:| |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:|||| |||||||||||:|||||| ||||:|| ::|:|||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| :||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| |||:| :| ||||||| ||| |||| | |||::||||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 8
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 78
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-78

  Query Match           76.5%;  Score 1888;  DB 4;  Length 465;
  Best Local Similarity  76.9%;  Pred. No. 2.9e-186;
  Matches  359;  Conservative   35;  Mismatches   71;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  ||||| |||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              :::  :|| ||:| |||:|||||||||| || |  :: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||:|||||||||||:|||||||:|||||| :|||.|||||||||| ||||:|||
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||  :|||||||:|| || |:|||:| |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:|||| |||||||||||:|||||| ||||:|| ::|:|||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| :||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| |||:| :| ||||||| ||| |||| | |||::||||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:|||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ::|  :|| ||:| |||:|||||||||| || |  :: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 180
              |||:|||||||||||:|||||||:|||||| :|||.|||||||||| ||||:|||
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||  :|||||||:|| || |:|||:| |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238


RESULT 9
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
;  APPLICANT:  Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION:  Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Sam
;  FILE REFERENCE:  GC586-2
;  CURRENT APPLICATION NUMBER: US/09/636,499
;  CURRENT FILING DATE:  2000-08-11
;  PRIOR APPLICATION NUMBER:  US 60/148,960
;  PRIOR FILING DATE:  1999-08-13
;  NUMBER OF SEQ ID NOS:  34
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-636-499-6

  Query Match           76.5%;  Score 1888;  DB 4;  Length 465;
  Best Local Similarity  76.9%;  Pred. No. 2.9e-186;
  Matches  359;  Conservative   35;  Mismatches   71;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  ||||| |||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
              ::|  :|| ||:| |||:|||||||||| || |  :: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:|||||||:|||||| :|||.|||||||||| ||||:|||
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||  :|||||||:|| || |:|||:| |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238
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Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
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RESULT 10
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-273-871A-8

Query Match 76.5%; Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%; Pred. No. 2.9e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
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RESULT 11
US-09-044-718-80
; Sequence 80, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-80

Query Match 76.2%; Score 1880; DB 4; Length 465;
Best Local Similarity 76.7%; Pred. No. 2e-185;
Matches 358; Conservative 35; Mismatches 72; Indels 2; Gaps 2;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
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RESULT 12
US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-79

  Query Match             76.1%;  Score 1879;  DB 4;  Length 465;
  Best Local Similarity   76.7%;  Pred. No. 2.5e-185;
  Matches  358;  Conservative   35;  Mismatches   72;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
              |     ||: | |       |    | | |||||| |||| |  ||||| ||||||  ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
               ::|  :|| ||:| |||||||||||||| || |  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
              |||:|||||||||||:|:|||||||:||||||| :|||||||||||||| |||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||  :|||||||:|| || |:|||:| ||||:||| :|
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              |. | ||||| |||||||:|||||  |||||||||||:||||| |:|||:|| :|:|||:||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              |||||||:|||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||:|||||: || |||||  :| |||||| ||| |||| | ||:::||||
Db        359 HDNSMVSIFFALGLYNGTEGLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| :|||||||  :|||:|||:|||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 13
US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-3

  Query Match             76.1%;  Score 1878.5;  DB 4;  Length 439;
  Best Local Similarity   79.8%;  Pred. No. 2.6e-185;
  Matches  351;  Conservative   35;  Mismatches   53;  Indels    1;  Gaps    1;

Qy         28 SHSCDTVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 87
              | |||||| |||| |  |||| ||| ||| || ::|  :|| ||:| ||||||||||
Db          1 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 60

Qy         88 TSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRY 147
              ||| || |  |: ||| ||| ||||:|||||||||||||||||||,|:|||||||::|
Db         61 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 120

Qy        148 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYN 207
              ||||| :|||||||||||||| |||||||| ||||||:||  ::|:| |:||||   :|
Db        121 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGAT-NRAAPAISVIIPESETFN 179

Qy        208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFD 267
              ||||||:|| || |:|||:| |||||:||| |||| | ||||| |||||||:|||| ||
Db        180 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFD 239

Qy        268 TVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
              ||||||||:|||||| ||||:|| :|:|||||||||||||||||||||:|| |'|||||
Db        240 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 299

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE 387
              | |||||||||| || ||||||||||:| |||||:|||||||||||||:||| ||||
Db        300 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 359

Qy        388 SIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
              | :| ||||||, ||| |||| | |||::||||||| |:|||||||||| |||||||| :
Db        360 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 419

Qy        448 DFVEGLSFARSGGNWEECFA 467
              |||:|||:|||||| |||:
Db        420 DFVKGLSWARSGGNWGECFS 439


RESULT 14
US-09-044-718-12
; Sequence 12, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
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;  ORGANISM: Aspergillus fumigatus
US-09-044-716-12

  Query Match           76.1%;  Score 1878.5;  DB 4;  Length 449;
  Best Local Similarity  79.8%;  Pred. No. 2.6e-185;
  Matches  351;  Conservative   35;  Mismatches   53;  Indels    1;  Gaps    1;

Qy         28 SHSCDIVDGGYQCFPEISHLWGTYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 87
Db         11 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 70

Qy         88 TSSASKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRY 147
Db         71 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 130

Qy        148 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYN 207
Db        131 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGAT-NRAAPAISVIIPESETFN 189

Qy        208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFD 267
Db        190 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFD 249

Qy        268 TVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
Db        250 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 309

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGIKPLSTTSVE 387
Db        310 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 369

Qy        388 SIEETDGYSASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
Db        370 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 429

Qy        448 DFVEGLSFARSGGNWEECFA 467
Db        430 DFVKGLSWARSGGNWGECFS 449


RESULT 15
US-09-044-718-81
; Sequence 81, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-81

  Query Match           76.0%;  Score 1876;  DB 4;  Length 465;
  Best Local Similarity  76.4%;  Pred. No. 5.1e-185;
  Matches  357;  Conservative   36;  Mismatches   72;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGTYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTAFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNILDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAKKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYSASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


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Delop 6.0 , Delext 7.0

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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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SUMMARIES

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2	1888	75.9	465	14	US-10-083-452-8	Sequence 8, Appli
3	1888	75.9	465	15	US-10-062-848-78	Sequence 78, Appl
4	1888	75.9	465	15	US-10-229-358-6	Sequence 6, Appli
5	1881.5	75.7	474	15	US-10-213-990-24	Sequence 24, Appl
6	1880	75.6	465	15	US-10-062-848-80	Sequence 80, Appl
7	1879	75.6	465	15	US-10-062-848-79	Sequence 79, Appl
8	1878.5	75.6	439	15	US-10-062-848-3	Sequence 3, Appli
9	1878.5	75.6	449	15	US-10-062-848-12	Sequence 12, Appl
10	1876	75.5	465	15	US-10-062-848-81	Sequence 81, Appl
11	1854	74.6	469	15	US-10-062-848-82	Sequence 82, Appl
12	1848	74.3	467	15	US-10-079-709-32	Sequence 32, Appl
13	1848	74.3	467	15	US-10-229-358-5	Sequence 5, Appli
14	1841	74.1	467	9	US-09-929-060-3	Sequence 3, Appli
15	1836	73.9	467	14	US-10-083-452-11	Sequence 11, Appl
16	1829	73.6	462	15	US-10-229-358-12	Sequence 12, Appl
17	1806	72.6	444	15	US-10-062-848-1	Sequence 1, Appli
18	1804.5	72.6	463	14	US-10-083-452-10	Sequence 10, Appl
19	1799	72.4	443	9	US-09-929-060-1	Sequence 1, Appli
20	1794	72.2	443	9	US-09-929-060-2	Sequence 2, Appli
21	1789.5	72.0	447	15	US-10-062-848-6	Sequence 6, Appli
22	1752	70.5	466	14	US-10-083-452-12	Sequence 12, Appl
23	1752	70.5	466	15	US-10-229-358-7	Sequence 7, Appli
24	1748	70.3	450	15	US-10-062-848-15	Sequence 15, Appl
25	1710	68.8	466	14	US-10-083-452-13	Sequence 13, Appl
26	1706.5	68.6	450	15	US-10-062-848-9	Sequence 9, Appli
27	1697	68.3	438	15	US-10-062-848-2	Sequence 2, Appli
28	1658	66.7	489	15	US-10-229-358-4	Sequence 4, Appli
29	1658	66.7	489	15	US-10-229-358-10	Sequence 10, Appl
30	1623	65.3	410	15	US-10-229-358-11	Sequence 11, Appl
31	1381	55.6	475	14	US-10-083-452-14	Sequence 14, Appl
32	1339	53.9	355	15	US-10-229-358-15	Sequence 15, Appl
33	1334.5	53.7	487	14	US-10-083-452-15	Sequence 15, Appl
34	1334.5	53.7	487	15	US-10-229-358-8	Sequence 8, Appli
35	1215	48.9	495	14	US-10-083-452-2	Sequence 2, Appli
36	1210	48.7	478	14	US-10-083-452-3	Sequence 3, Appli
37	920	37.0	284	15	US-10-229-358-19	Sequence 19, Appl
38	867	34.9	283	15	US-10-229-358-9	Sequence 9, Appli
39	867	34.9	283	15	US-10-229-358-24	Sequence 24, Appl
40	845.5	34.0	443	14	US-10-083-452-5	Sequence 5, Appli
41	833.5	33.5	453	14	US-10-083-452-6	Sequence 6, Appli
42	830.5	33.4	439	14	US-10-083-452-7	Sequence 7, Appli
43	825	33.2	442	14	US-10-083-452-4	Sequence 4, Appli
44	729.5	29.3	212	15	US-10-229-358-16	Sequence 16, Appl
45	406	16.3	312	15	US-10-229-358-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25

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;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Variation
US-10-083-452-9

Alignment Scores:
Pred. No.:              2.79e-181       Length:         467
Score:                  2308.00         Matches:        436
Percent Similarity:     95.72%          Conservative:   11
Best Local Similarity:  93.36%          Mismatches:     20
Query Match:            92.84%          Indels:         0
DB:                     14              Gaps:           0

US-09-488-265B-30 (1-1404) x US-10-083-452-9 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              ||||||||||||||||||||||||||||||   ||||||||||:::||||||||||   ||||||
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ||||||||||||||||||||||||      ||||||||||| |||||||||||||||||||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTACAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||:::   ||||||||||||||||||||||||:::||||||||||
Db        181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||||||:::||||||||||||||||||||||||||   ||||||||||||||:::
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||||   ||||||
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||||||||||   ||||||||||||   ||||||||||||||||||||   |||
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||||||||:::||||||||||||||||||||||||||||||:::||||||||||
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   ||||||||||||||||||||||   ||||||||||||||||||||||||||
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              ||||||||||:::|||:::||||||||||||||||||||||||||||||||   |||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              ||||||||||   ||||||||||||||||||||||||||||||:::||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              ||||||||||||||||:||||||||||||||||||||||||||||||||   ||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   ||||||||||||
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 2
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
;  APPLICANT: Svendsen, Allan
;  TITLE OF INVENTION: Phytase Variants
;  FILE REFERENCE: 5618.500-US
;  CURRENT APPLICATION NUMBER: US/10/083,452
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: US/09/273,871
;  PRIOR FILING DATE: 1999-03-22
;  PRIOR APPLICATION NUMBER: PA 1998 00407
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: PA 1998 00806
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: PA 1998 01176
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: PA 1999 00091
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/080,129
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/090,675
;  PRIOR FILING DATE: 1998-06-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
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US-10-083-452-8

Alignment Scores:

Pred. No.:	9.97e-147	Length:	465
Score:	1888.00	Matches:	359
Percent Similarity:	84.37%	Conservative:	35
Best Local Similarity:	76.87%	Mismatches:	71
Query Match:	75.95%	Indels:	2
DB:	14	Gaps:	2

US-09-488-265B-30 (1-1404) x US-10-083-452-8 (1-465)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||                 |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           |||   |||  ||||||||||||||||||   ||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
                 |||      |||||||||||||||   ||||||||||||||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
                 ::::::|||      :::||||||   ||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||||   ||||||   |||      ||||::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   |||||||||   ||||||||||||:::||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::||||||||||||||||||||   :::||||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||||      :::::|||:::|||   |||:::|||:|||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||         :::|||||||||||||||||||||||:::|||||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||:::|||||||||:::|||   ||||||||||||||:::||||||||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   |||   |||||||||||||||   |||||||||||||||||.|:::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   |||||||||||:::|||||   :::|||:::|||||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   |||||||||||||||||||||||||||||||'|||:::|||   ||||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              ||||||||||:::|||'||||||||||||||:|||||||||||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||||||||||||   :::|||   ||||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              ||||||||   |||||||||||   |||   ||||||||:::::|||||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              ||||||||   |||:::|||||||||||||||||||||||||||||   ||||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   :::|||||||||:::|||||||||:::|||||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   ||||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465
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RESULT 3
US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-78

Alignment Scores:

Pred. No.:	9.97e-147	Length:	465
Score:	1888.00	Matches:	359
Percent Similarity:	84.37%	Conservative:	35
Best Local Similarity:	76.87%	Mismatches:	71
Query Match:	75.95%	Indels:	2
DB:	15	Gaps:	2

US-09-488-265B-30 (1-1404) x US-10-062-848-78 (1-465)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
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Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTC 780
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        339 ThrLeuValSerAsnProAlaThrProProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465
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RESULT 4
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Alignment Scores:

Pred. No.:	9.97e-147	Length:	465
Score:	1888.00	Matches:	359
Percent Similarity:	84.37%	Conservative:	35
Best Local Similarity:	76.87%	Mismatches:	71
Query Match:	75.95%	Indels:	2
DB:	15	Gaps:	2

US-09-488-265B-30 (1-1404) x US-10-229-358-6 (1-465)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
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```
Db        80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy       301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db       100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy       361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db       120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy       421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db       140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy       481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db       160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy       541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTAIT 600
Db       180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy       601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db       199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy       661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db       219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy       721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db       239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy       781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db       259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy       841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db       279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy       901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db       299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy       961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db       319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy      1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db       339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy      1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db       359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy      1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db       379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy      1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db       399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy      1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db       419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy      1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db       439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy      1381 AACTGGGAAGAATGTTTCGCT 1401
Db       459 AsnTrpGlyGluCysPheSer 465
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RESULT 5
US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-24

Alignment Scores:

Pred. No.:	3.44e-146	Length:	474
Score:	1881.50	Matches:	355
Percent Similarity:	84.76%	Conservative:	40
Best Local Similarity:	76.18%	Mismatches:	64
Query Match:	75.68%	Indels:	7
DB:	15	Gaps:	2

US-09-488-265B-30 (1-1404) x US-10-213-990-24 (1-474)

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Qy          4 GGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACCGCC 63
Db         16 GlyAlaValValLeuIleLeuLysArgSerArgValSerAlaAlaProSerSer------ 33

Qy         64 TTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTC 123
Db         34 ------------AlaGlySerLysSerCysAspThrValAspLeuGlyTyrGlnCysSer 49

Qy        124 CCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCT 183
Db         50 ProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeu 69

Qy        184 GCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGA 243
Db         70 SerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSerArg 89

Qy        244 CACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCT 303
Db         90 HisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThrAla 109

Qy        304 ATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTAC 363
Db        110 IleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyr 129

Qy        364 ACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATT 423
Db        130 ThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIle 149

Qy        424 AAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCT 483
Db        150 LysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAlaSer 169

Qy        484 GGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAG 543
Db        170 GlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLys 189
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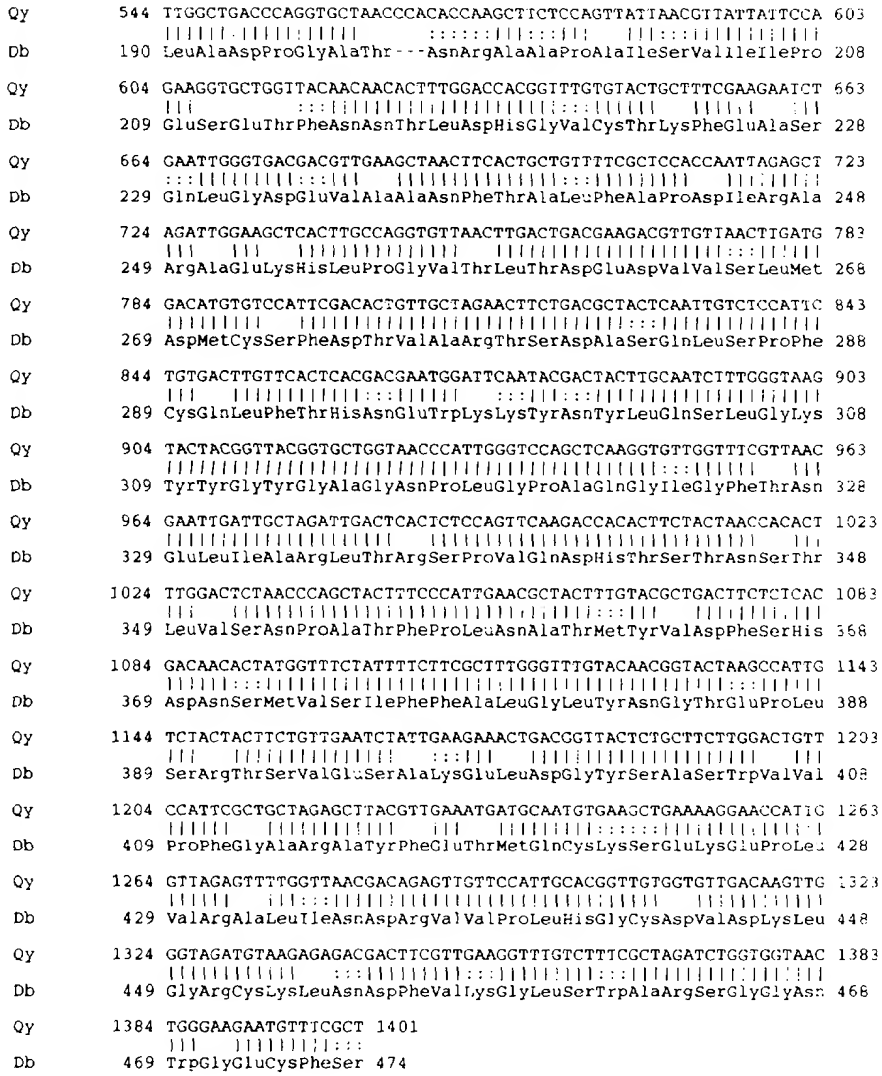

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Qy        544 TTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCA 603
Db        190 LeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIlePro 208

Qy        604 GAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAAICT 663
Db        209 GluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAlaSer 228

Qy        664 GAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCT 723
Db        229 GlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAla 248

Qy        724 AGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATG 783
Db        249 ArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeuMet 268

Qy        784 GACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTC 843
Db        269 AspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerProPhe 288

Qy        844 TGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAG 903
Db        289 CysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLys 308

Qy        904 TACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAAC 963
Db        309 TyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsn 328

Qy        964 GAATTGATTGCTAGATTGACTCACICTCCAGTTCAAGACCACACTTCTACTAACCACACT 1023
Db        329 GluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSerThr 348

Qy       1024 TTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCAC 1083
Db        349 LeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSerHis 368

Qy       1084 GACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTG 1143
Db        369 AspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeu 388

Qy       1144 TCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTT 1203
Db        389 SerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValVal 408

Qy       1204 CCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATIG 1263
Db        409 ProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluProLeu 428

Qy       1264 GTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTG 1323
Db        429 ValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLysLeu 448

Qy       1324 GGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAAC 1383
Db        449 GlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsn 468

Qy       1384 TGGGAAGAATGTTTCGCT 1401
Db        469 TrpGlyGluCysPheSer 474
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```
RESULT 6
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-80

Alignment Scores:
Pred. No.:                4.54e-146      Length:          465
Score:                    1880.00        Matches:         358
Percent Similarity:       84.15%         Conservative:    35
Best Local Similarity:    76.66%         Mismatches:      72
Query Match:              75.62%         Indels:          2
DB:                       15             Gaps:            2

US-09-488-265B-30 (1-1404) x US-10-062-848-80 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
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Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 7
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-79
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Alignment Scores:
Pred. No.:                5.48e-146       Length:          465
Score:                    1879.00         Matches:         358
Percent Similarity:       84.15%          Conservative:    35
Rest Local Similarity:    76.66%          Mismatches:      72
Query Match:              75.58%          Indels:          2
DB:                       15              Gaps:            2

US-09-488-265B-30 (1-1404) x US-10-062-848-79 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
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Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              |||||  ||||||||||||||||||||||||||||||||||:::|||  |||||.|||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||:::
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||  ||||||||||||||||  :::|||  |||.|||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              ||||||||  ||||||||||||  |||  |||||||||:::::|||||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||  |||:::|||||||||||||||||||||||||||||||  ||||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||  :::|||||||||:::|||||||||:::|||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||  ||||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 8
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-3

Alignment Scores:
Pred. No.:              5.9e-146        Length:         439
Score:                  1878.50         Matches:        351
Percent Similarity:     87.73%          Conservative:   35
Best Local Similarity:  79.77%          Mismatches:     53
Query Match:            75.56%          Indels:         1
DB:                     15              Gaps:           1

US-09-488-265B-30 (1-1404) x US-10-062-848-3 (1-439)

Qy         82 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 141
              |||  ||||||||||||||||||  ||||||||||||  |||      |||||||||

Db          1 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 20

Qy        142 TGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGTT 201
              ||||||  ||||||||||||||||||||  ||||||  :::::::||      :::
Db         21 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 40

Qy        202 CCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 261
              ||||||  ||||||:::|||  ||||||||||||||||||||||||||||||||||||
Db         41 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 60

Qy        262 ACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 321
              |||||||||  ||||||  |||:::  ||||||||||  |||||||||
Db         61 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 80

Qy        322 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 381
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db         81 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 100

Qy        382 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 441
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||:::||||
Db        101 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 120

Qy        442 AAGGCTTTGGCTAGAAAGATIGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTATT 501
              ||||||||||||||  :::|||||||||||||||||||||||||||||||||||||||||
Db        121 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 140

Qy        502 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTGCT 561
              ||||||  ||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        141 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 160

Qy        562 AACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAAC 621
                  ::::::|||:::|||  |||:::|||||||||||||||||        :::|||
Db        161 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 179

Qy        622 AACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTT 681
              ||||||||||||||||||:::||||||  ||||||  |||:::|||||||||:::|||
Db        180 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 199

Qy        682 GAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTG 741
              ||||||||||||||||:::|||||||||  ||||||||||||  |||  ||||||
Db        200 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 219

Qy        742 CCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGAC 801
              |||||||||  ||||||||||||||||||||:::|||||||||||||||  ||||||
Db        220 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 239

Qy        802 ACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACTCAC 861
              ||||||||||||||||||||||:::|||||||||||||||||||  ||||||||||||
Db        240 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 259

Qy        862 GACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCT 921
              :::||||||  :::|||:::|||||||||||||||||||||||||||||||||||||||
Db        260 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 279

Qy        922 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTG 981
              ||||||||||||||||||||||||||:::||||||  ||||||||||||||||||||
Db        280 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 299

Qy        982 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1041
              |||  ||||||||||||||||||||||||||||||  ||||||  ||||||||||||
Db        300 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 319

Qy       1042 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTCT 1101
              ||||||||||||||||||||||:::|||  ||||||||||||||||||:::||||||||||
Db        320 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 339

Qy       1102 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTTGAA 1161
              ||||||||||||||||||||||||||||||||||:::|||||||||  ||||||||||||
Db        340 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 359

Qy       1162 TCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1221
              |||  :::|||  ||||||||||||||||||||  |||||||||  |||||||||
Db        360 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 379
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Qy       1222 TACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1281
Db        380 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 399

Qy       1282 GACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1341
Db        400 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 419

Qy       1342 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGCT 1401
Db        420 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 439

RESULT 9
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Alignment Scores:
Pred. No.:                5.95e-146      Length:          449
Score:                    1878.50        Matches:         351
Percent Similarity:       87.73%         Conservative:    35
Best Local Similarity:    79.77%         Mismatches:      53
Query Match:              75.56%         Indels:          1
DB:                       15             Gaps:            1

US-09-488-265B-30 (1-1404) x US-10-062-848-12 (1-449)

Qy         82 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 141
Db         11 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 30

Qy        142 TGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGTT 201
Db         31 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 50

Qy        202 CCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 261
Db         51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70

Qy        262 ACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 321
Db         71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90

Qy        322 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 381
Db         91 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110

Qy        382 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 441
Db        111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130

Qy        442 AAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTATT 501
Db        131 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 150

Qy        502 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTGCT 561
Db        151 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 170

Qy        562 AACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAAC 621
Db        171 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189

Qy        622 AACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTT 681
Db        190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209

Qy        682 GAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTG 741
Db        210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 229

Qy        742 CCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGAC 801
Db        230 ProGlyValThrLeuThrAspGluAspValSerLeuMetAspMetCysSerPheAsp 249

Qy        802 ACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACTCAC 861
Db        250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269

Qy        862 GACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCT 921
Db        270 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 289

Qy        922 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTG 981
Db        290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309

Qy        982 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1041
Db        310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329

Qy       1042 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTCT 1101
Db        330 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 349

Qy       1102 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTTGAA 1161
Db        350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 369

Qy       1162 TCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1221
Db        370 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 389

Qy       1222 TACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1281
Db        390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409

Qy       1282 GACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1341
Db        410 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 429

Qy       1342 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGCT 1401
Db        430 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 449

RESULT 10
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
```

```
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Alignment Scores:
Pred. No.:                9.68e-146      Length:          465
Score:                    1876.00        Matches:         357
Percent Similarity:       84.15%         Conservative:    36
Best Local Similarity:    76.45%         Mismatches:      72
Query Match:              75.46%         Indels:          2
DB:                       15             Gaps:            2

US-09-488-265B-30 (1-1404) x US-10-062-848-81 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||                 |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
                 |||      ||||||||||||||||   ||||||||||||||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
                 :::::|||      :::|||||   |||,|||:|||   |||||.||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||   ||||||   |||      ||||:
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   |||||||||   |||||||||||:|:::|||||:|||||:||| ||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||   ||||||||||||:|:::||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrAlaPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||||||||||||||   :::||||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAlaAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||||      :::::|||:::|||   |||:::|||||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||         :::||||||||||||||||||||:::||||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||:::|||||||||||:::|||   |||:|||||:|||||:::||||,||||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   :::   ||||||||||||||||   ||||||||||||||||||||:::|||
Db        239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   |||||||||:|||||||||||||||||||:::|:||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   ||||||||||||:::|||||   :::|||:::|||||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||,|||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   ||||||||||||||||||||||||||||||||||:::|||   ||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||||||||||||||||||||||||||||||||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||||||||||||   :::|||   ||||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||   ||||||||||||   |||   ||||||||||:::::||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||   |||:::|||||||||||||||||||||||||||||||   |||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||,|||||||   :::||||||||||:::|||||||||:::||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   ||||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 11
US-10-062-848-82
; Sequence 82, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
```

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; SEQ ID NO 82
;   LENGTH: 469
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-82

Alignment Scores:
Pred. No.:              6.27e-144       Length:         469
Score:                  1854.00         Matches:        347
Percent Similarity:     84.47%          Conservative:   50
Best Local Similarity:  73.83%          Mismatches:     69
Query Match:            74.58%          Indels:         4
DB:                     15              Gaps:           2

US-09-488-265B-30 (1-1404) x US-10-062-848-82 (1-469)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGT--- 57
              ||||||          |||||||||||:::     |||          :::|||
Db          1 MetGlyAlaLeuThrPheLeuLeuSerValMetTyrLeuLeuSerGlyValAlaGlyAla 20

Qy         58 ------ACCGCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGT 111
                    :::                     |||   :::|||||:|||||:::   : |
Db         21 ProSerSerGlyCysSerAlaGlySerGlySerLysAlaCysAspThrValGluLeuGly 40

Qy        112 TACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTG 171
              |||||||||   |.|      |||||||||||||||   ||||||.|||||.||| |||
Db         41 TyrGlnCysSerProGlyThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeu 60

Qy        172 GCTGACGAATCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAA 231
                :|||||   :::::::|||   |||:::||||||   |||||||||||||.|||||||
Db         61 GluAspGluLeuSerValSerSerAspLeuProLysAspCysArgValThrPheValGln 80

Qy        232 GTTTTGTCTAGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCT 291
              |||||||||||||||||||||||||||||||:::|||   ||||||   |:|
Db         81 ValLeuSerArgHisGlyAlaArgTyrProThrAlaSerLysSerLysLysTyrLysLys 100

Qy        292 TTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAG 351
              |||:::   ||||||||||||||||||||   ||||||||||||:::|||||||||:::
Db        101 LeuValThrAlaIleGlnLysAsnAlaThrGluPheLysGlyLysPheAlaPheLeuGlu 120

Qy        352 ACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTT 411
              |||||||||||||||||||||||||||||||||||||:|||||||||||||:|||||||
Db        121 ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnMetVal 140

Qy        412 AACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTC 471
              |||||||||||||||||||||:::::|||||||||||||||||      :::|||||||||
Db        141 AsnSerGlyIleLysPheTyrGlnLysTyrLysAlaLeuAlaGlySerValValProPhe 160

Qy        472 ATTAGAGCTTCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTC 531
              ||||||:::|||||||||||||||||||||||||||   ||||||||||||:|||||||
Db        161 IleArgSerSerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPhe 180

Qy        532 CAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC 591
              |||   |||   :::|||||| |||||||||      :::::::|||:::|||||||:::
Db        181 GlnGlnAlaAsnValAlaAspProGlyAlaThr---AsnArgAlaAlaProValIleSer 199

Qy        592 GTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCT 651
              ||||||||||||||         |||||||||:|||||||   :::|||||
Db        200 ValIleIleProGluSerGluThrTyrAsnAsnThrLeuAspHisSerValCysThrAsn 219

Qy        652 TTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGGTCCA 711
              ||||||   |||||||||||||||:::||||||||||||||||||||:::|||||||||
Db        220 PheGluAlaSerGluLeuGlyAspGluValGluAlaAsnPheThrAlaLeuPheAlaPro 239

Qy        712 CCAATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTT 771
                |||||||||||||:::|||   |||||||||||||||   ||||||||:::|||||
Db        240 AlaIleArgAlaArgIleGluLysHisLeuProGlyValGlnLeuThrAspAspAspVal 259

Qy        772 GTTAACTTGATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAA 831
              |||:::|||||||||||||||   |||||||||||||||||||:::|||||||||||||
Db        260 ValSerLeuMetAspMetCysSerPheAspThrValAlaArgThrAlaAspAlaSerGlu 279

Qy        832 TTGTCTCCATTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAA 891
              |||:|||||||||||||||   |||||||||||||||||||:::|||||||||||||||
Db        280 LeuSerProPheCysAlaIlePheThrHisAsnGluTrpLysLysTyrAspTyrLeuGln 299

Qy        892 TCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTT 951
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        300 SerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIle 319

Qy        952 GGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCT 1011
              ||||||   |||||||||||||||||||||||||:::|||||||||||||||||||:::|||
Db        320 GlyPheThrAsnGluLeuIleAlaArgLeuThrAsnSerProValGlnAspHisThrSer 339

Qy       1012 ACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCT 1071
              ||||||   ||||||||||||:::|||||||||||||||||||||||||||:::|||
Db        340 ThrAsnSerThrLeuAspSerAspProAlaThrPheProLeuAsnAlaThrIleTyrVal 359

Qy       1072 GACTTCTCTCACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGT 1131
              ||||||||||||||||||   |||:::   |||||||||||:::|||||||||||||||
Db        360 AspPheSerHisAspAsnGlyMetIleProIlePhePheAlaMetGlyLeuTyrAsnGly 379

Qy       1132 ACTAAGCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCT 1191
              ||:::|||||||||   ||||||   ||||||   :::|||:::::::|||||||||||
Db        380 ThrGluProLeuSerGlnThrSerGluGluSerThrLysGluSerAsnGlyTyrSerAla 399

Qy       1192 TCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAAATGTGAAGCTGAA 1251
              ||||||   ||||||||   ||||||||||||   |||   ||||||||:::::::|||
Db        400 SerTrpAlaValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlu 419

Qy       1252 AAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGT 1311
              ||||||||||||:|||||   |||:::|||||||||||||||||||||||||||||||||
Db        420 LysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAla 439

Qy       1312 GTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGA 1371
              ||||||||||||||||||||||||      ||||||||:::|||||||||:::||||||
Db        440 ValAspLysLeuGlyArgCysLysLeuLysAspPheValLysGlyLeuSerTrpAlaArg 459

Qy       1372 TCTGGTGGTAACTGGGAAGAATGTTTCGCT 1401
              ||||||||||||   ||||::   ||||::
Db        460 SerGlyGlyAsnSerGluGlnSerPheSer 469

RESULT 12
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/079,709
;      FILING DATE:  02-FEB-2002
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/233,510
;      FILING DATE:  20-JAN-1999
```

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;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-079-709-32

Alignment Scores:
Pred. No.:              1.95e-143     Length:          467
Score:                  1848.00       Matches:         347
Percent Similarity:     83.30%        Conservative:    42
Best Local Similarity:  74.30%        Mismatches:      78
Query Match:            74.34%        Indels:          0
DB:                     15            Gaps:            0

US-09-488-265B-30 (1-1404) x US-10-079-709-32 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||||||||      |||||||||   :::      |||   |||   |||||||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||:::            |||      ||||||||||||||||||   ||||||||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              |||   |||   ||||||||||||||   |||:::|||||||||||||||||:::|||||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||   |||||||||:::|||||   ||||||||||||||||||   ||||||||:|||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||   |||      |||   |||||||||| |||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||:::|||||||||   |||   ||||.||||.|||||||||; |||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              |||:::|||||:|:|||'|:||||:|||||||||||||||||:::::|||||||||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||:::|||||:::::|||   |||   ||||||||||||||||:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||   ||||||||||||||   :::|||||||||||||||||||:|||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||   ||||||   |||   |||   |||:::||||||   |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              |||   :::      |||||||||||||||   |||   ||||||   |||||||:::
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||||||||   |||   |||||||||||||||||||||   |||   |||   ||||||

Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              |||||||||      |||   ||||||   ||||||||   :::|||      |||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   ||||||||||:::::   :::::      |||:::||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||:::||||||||:||||||||||:|||   ||||||||||||:::
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||   |||   ||||||:::||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||:::||||||||||||||||||||||||:::||||||||||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||   ::::::||||||   ||||||||||||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||:::||||||||:|||   :::||||||||||:::||||:::||||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||||||:::|||   ||||||||||||||||||||||:::||||||:::||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||||||||||||||||||||||||||||'||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              |||||||||||   ||||||   ||||||   ||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              :::|||   ||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 13
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-229-358-5
```

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Alignment Scores:
Pred. No.:                1.95e-143      Length:          467
Score:                    1848.00        Matches:         347
Percent Similarity:       83.30%         Conservative:    42
Best Local Similarity:    74.30%         Mismatches:      78
Query Match:              74.34%         Indels:          0
DB:                       15             Gaps:            0

US-09-488-265B-30 (1-1404) x US-10-229-358-5 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||||||||      |||||||||   :::      |||   |||   |||||||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||:::          |||       |||||||||||||||||   |||||||||  ||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              |||   |||   |||||||||||||||   |||:::|||||||||||||||||||:::|||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||   |||||||||:::|||||   |||||||||||||||||   |||||||||||:
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||:|||||||||||   |||      |||   ||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
                 |||||:::|||||||||:   |||   |||||||||||||||||||||||||||:|||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              |||:::|||||||||||||||||||||||||||||||||||:::::||||||, ||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||:::::|||   |||   |||||||||||||||||:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||   |||||||||||||||||   :::|||||||||||||||||||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||   ||||||   |||   |||   |||:::|||||   |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
                 |||   :::      |||||||||||||||   |||   ||||||   |||||||:::
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||||||||   |||   ||||||||||||||||||||   |||   |||   ||||||
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
                 |||||||||      |||   ||||||   ||||||||   :::|||      |||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||   |||||||||::::::   ::::::      |||:::|||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||:::|||||||||||||||||||   ||||||||||||:::
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||||||||   |||   ||||||:::||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||:::|||||||||||||||||||||||:::|||||||||||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||   ::::::|||||   ||||||||||||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||:::|||||||:::|||   :::|||||||||:::|||||||||||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||||:::|||   ||||||||||||||||||||:::|||||:::||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   ||||||   ||||||   ||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              :::|||   ||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 14
US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
;  APPLICANT: KONDO, HIDEMASA
;  APPLICANT:  ANAZAWA, HIDEHARU
;  APPLICANT:  KANEKO, SYUNICHI
;  APPLICANT:  NAGASHIMA, TADASHI
;  APPLICANT:  TANGE, TATSUYA
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 081356/0166
;  CURRENT APPLICATION NUMBER: US/09/929,060
;  CURRENT FILING DATE:  2001-08-05
;  PRIOR APPLICATION NUMBER: 09/543,744
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: 09/155,855
;  PRIOR FILING DATE: 1998-10-05
;  PRIOR APPLICATION NUMBER: JP 084314/1996
;  PRIOR FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-929-060-3

Alignment Scores:
Pred. No.:                7.34e-143      Length:          467
Score:                    1841.00        Matches:         342
Percent Similarity:       83.73%         Conservative:    49
Best Local Similarity:    73.23%         Mismatches:      76
Query Match:              74.05%         Indels:          0
DB:                       9              Gaps:            0

US-09-488-265B-30 (1-1404) x US-09-929-060-3 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||||||||      |||||||||   :::      |||   |||   |||||||||
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Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnLys 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         61 SerAlaIleSerProAspValProAlaGlyCysHisValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        141 ValLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        161 SerGlySerSerArgValIleAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIleIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        201 SerGluAlaSerThrSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        221 SerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValSerLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        281 PheCysAspLeuPheThrHisGluGluTrpIleAsnTyrAspTyrLeuGlnSerLeuAsn 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerSerThrThrAlaGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        401 ValProPheAlaSerArgMetTyrValGluMetMetGlnCysGlnSerGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        441 LeuGlyArgCysThrArgAspSerPheValLysGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        461 AspTrpGlyGluCysPheAla 467

RESULT 15
US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
;  APPLICANT: Svendsen, Allan
;  TITLE OF INVENTION: Phytase Variants
;  FILE REFERENCE: 5618.500-US
;  CURRENT APPLICATION NUMBER: US/10/083,452
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: US/09/273,871
;  PRIOR FILING DATE: 1999-03-22
;  PRIOR APPLICATION NUMBER: PA 1998 00407
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: PA 1998 00806
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: PA 1998 01176
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: PA 1999 00091
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/080,129
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/090,675
;  PRIOR FILING DATE: 1998-06-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus ficuum
US-10-083-452-11

Alignment Scores:
Pred. No.:              1.89e-142       Length:         467
Score:                  1836.00         Matches:        345
Percent Similarity:     82.87%          Conservative:   42
Best Local Similarity:  73.88%          Mismatches:     80
Query Match:            73.85%          Indels:         0
DB:                     14              Gaps:           0

US-09-488-265B-30 (1-1404) x US-10-083-452-11 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
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Db        41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy       181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
             |||   |||||||||:::|||||   ||||||||||||||||||   ||||||||||||
Db        61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy       241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
             |||||||||||||||||||||||   |||      |||   ||||||||||||||||||
Db        81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy       301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
             ||||||:::|||||||||   |||   ||||||||||||||||||||||||||||||||
Db       101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy       361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
             |||:::|||||||||||||||||||||||||||||||||||||:::::|||||| |||.
Db       121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy       421 ATTAAGTICTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
             |||||||:|||||:::|||||:::::::|||   |||   ||||||||||||||||:|||:::
Db       141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy       481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
             |||||||||   ||||:|||||||||||   :::|||||||||||||:|||||||||||
Db       161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy       541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
             ||||||   ||||||   |||   |||   |||:::|:|||||   |||:::|||:::|||
Db       181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy       601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
             |||   :::      ||||||.|||||||   |||   |:|||   |||:::|||||
Db       201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy       661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
             |||||||||   |||   ||||||||||:|||||||||||   |||   |||   ||||||
Db       221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy       721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
             |||||||||      |||   ||||||   ||||||||    :::|||      |.|
Db       241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy       781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
             ||||||||||||   ||||:||||::::::   ::::::      |:|:::||||||||
Db       261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy       841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
             ||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy       901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
             ||||||||||||:::|||||||||||||||||||||||||   ||||||||||||:::
Db       301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy       961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
             ||||||||||||||||:|||||||||||||||||||||||   |||   ||||||:::|||||
Db       321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy      1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
             ||||||||||||:::|||||||||||||||||   :::|||||||||||||:|||||||
Db       341 ThrLeuAspSerSerProAlaThrPheProLeuLysSerThrLeuTyrAlaAspPheSer 360

Qy      1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
             |||||||||   ::::::||||||   ||||||||||||||||||||||||||||||||
Db       361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy      1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
             ||||||||||||:::|||||||:|||   :::|||||||||||:::|:::::::|||||
Db       381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy      1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
             ||||||||||||:::|||   |||||||||||||||||:::|||||||:::   |||
Db       401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnAlaPro 420

Qy      1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db       421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy      1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
             ||||||||||||   ||||||   ||||||   ||||||||||||||||||||||||||
Db       441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy      1381 AACTGGGAAGAATGTTTCGCT 1401
             :::|||   ||||||||||||
Db       461 AspTrpAlaGluCysPheAla 467
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Search completed: October 3, 2003, 09:06:16
Job time : 94.6311 secs

GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 07:48:21 ; Search time 21.0567 Seconds
(without alignments)
5642.336 Million cell updates/sec

Title: US-09-488-265B-30
Perfect score: 2486
Sequence: 1 atgggcgtgttcgtcgtgct.....gggaagaatgtttcgcttaa 1404

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09488265/runat_03102003_074813_12239/app_query.fasta_1.4693
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=oct3.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265_@CGN_1_1_99_@runat_03102003_074813_12239 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2308	92.8	467	4	US-09-273-871A-9	Sequence 9, Appli
2	2182	87.8	441	3	US-09-121-425-1	Sequence 1, Appli
3	2182	87.8	441	4	US-09-634-493A-1	Sequence 1, Appli
4	2170	87.3	467	3	US-09-121-425-2	Sequence 2, Appli
5	2170	87.3	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1888	75.9	465	3	US-08-868-435-33	Sequence 33, Appl
7	1888	75.9	465	4	US-08-744-231-33	Sequence 33, Appl
8	1888	75.9	465	4	US-09-044-718-78	Sequence 78, Appl
9	1888	75.9	465	4	US-09-636-499-6	Sequence 6, Appli
10	1888	75.9	465	4	US-09-273-871A-8	Sequence 8, Appli
11	1880	75.6	465	4	US-09-044-718-80	Sequence 80, Appl
12	1879	75.6	465	4	US-09-044-718-79	Sequence 79, Appl
13	1878.5	75.6	439	4	US-09-044-718-3	Sequence 3, Appli
14	1878.5	75.6	449	4	US-09-044-718-12	Sequence 12, Appl
15	1876	75.5	465	4	US-09-044-718-81	Sequence 81, Appl
16	1854	74.6	469	4	US-09-044-718-82	Sequence 82, Appl
17	1852	74.5	467	1	US-07-923-724-8	Sequence 8, Appli
18	1852	74.5	467	2	US-08-609-426A-8	Sequence 8, Appli
19	1852	74.5	467	2	US-08-374-652C-2	Sequence 2, Appli
20	1848	74.3	467	1	US-08-151-574-32	Sequence 32, Appl
21	1848	74.3	467	1	US-08-146-424-20	Sequence 20, Appl
22	1848	74.3	467	1	US-08-693-709-2	Sequence 2, Appli
23	1848	74.3	467	2	US-08-419-448-32	Sequence 32, Appl
24	1848	74.3	467	2	US-08-819-825-3	Sequence 3, Appli
25	1846	74.3	467	3	US-09-163-642-3	Sequence 3, Appli
26	1848	74.3	467	4	US-09-233-510-32	Sequence 32, Appl
27	1848	74.3	467	4	US-09-636-499-5	Sequence 5, Appli
28	1841	74.1	467	3	US-09-155-855-3	Sequence 3, Appli
29	1841	74.1	467	4	US-09-543-744-3	Sequence 3, Appli
30	1841	74.1	467	4	US-09-929-060-3	Sequence 3, Appli
31	1836	73.9	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1829	73.6	462	4	US-09-636-499-12	Sequence 12, Appl
33	1822	73.3	466	3	US-08-868-435-35	Sequence 35, Appl
34	1822	73.3	466	4	US-08-744-231-35	Sequence 35, Appl
35	1819	73.2	466	3	US-08-868-435-12	Sequence 12, Appl
36	1819	73.2	466	4	US-08-744-231-12	Sequence 12, Appl
37	1806	72.6	444	4	US-09-044-718-1	Sequence 1, Appli
38	1804.5	72.6	463	3	US-08-868-435-29	Sequence 29, Appl
39	1804.5	72.6	463	4	US-08-744-231-29	Sequence 29, Appl
40	1804.5	72.6	463	4	US-09-273-871A-10	Sequence 10, Appl
41	1799	72.4	443	3	US-09-155-855-1	Sequence 1, Appli
42	1799	72.4	443	4	US-09-543-744-1	Sequence 1, Appli
43	1799	72.4	443	4	US-09-929-060-1	Sequence 1, Appli
44	1794	72.2	443	3	US-09-155-855-2	Sequence 2, Appli
45	1794	72.2	443	4	US-09-543-744-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Alignment Scores:
Pred. No.: 7.66e-218 Length: 467
Score: 2308.00 Matches: 436
Percent Similarity: 95.72% Conservative: 11

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Best Local Similarity:  93.36%        Mismatches:    20
Query Match:            92.84%        Indels:        0
DB:                     4             Gaps:          0

US-09-488-265B-30 (1-1404) x US-09-273-871A-9 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              |||||||||||||||||||||||||||   ||||||||:::|||||||||   ||||||
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              |||||||||||||||||||||||||:||||   ||||||||||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:||||:|||||||||||:|||||||||||||||||||||||||||||
Db        141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||:::   |||||||||||||||||||||||:::|||||||||||
Db        181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              |||||||||:::|||||||||||||||||||||:||||   ||||||||||||||:::
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||||||||||||||||||||||||||||||||||||:::|||||||||   ||||||
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||||||||||   ||||||||||||   ||||||||||||||||||   |||
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||||||||:::||||||||||||||||||||||||||:::||||||||||
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   ||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              |||||||||||||||||||||||   ||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              ||||||||||:::|||:::|||||||||||||||||||||||||||||||||||   |||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||   ||||||||||||||||||||||||||||||:::|||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   ||||||||||||
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

Alignment Scores:
Pred. No.:              1.73e-205     Length:        441
Score:                  2182.00       Matches:       410
Percent Similarity:     95.46%        Conservative:  11
Best Local Similarity:  92.97%        Mismatches:    20
Query Match:            87.77%        Indels:        0
DB:                     3             Gaps:          0

US-09-488-265B-30 (1-1404) x US-09-121-425-1 (1-441)

Qy         79 AACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCAC 138
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Db          1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20

Qy        139 TTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGAC 198
              |||||||||   ||||||||:::|||||||||   ||||||||||||||||||||||||
Db         21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40

Qy        199 GTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATAC 258
              ||||||      ||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60
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Qy       259 CCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCT 318
Db        61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80

Qy       319 ACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
Db        81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

Qy       379 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGA 438
Db       101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120

Qy       439 TACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTT 498
Db       121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140

Qy       499 ATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGT 558
Db       141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160

Qy       559 GCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTAC 618
Db       161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180

Qy       619 AACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGAC 678
Db       181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

Qy       679 GTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCAC 738
Db       201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220

Qy       739 TTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTC 798
Db       221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240

Qy       799 GACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACT 858
Db       241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260

Qy       859 CACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGT 918
Db       261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280

Qy       919 GCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGA 978
Db       281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

Qy       979 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCA 1038
Db       301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320

Qy      1039 GCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTT 1098
Db       321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340

Qy      1099 TCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTT 1158
Db       341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360

Qy      1159 GAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGA 1218
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Qy      1219 GCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
Db       381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

Qy      1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGA 1338
Db       401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420

Qy      1339 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTC 1398
Db       421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440

Qy      1399 GCT 1401
Db       441 Ala 441
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RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-1

Alignment Scores:

Pred. No.:	1.73e-205	Length:	441
Score:	2162.00	Matches:	410
Percent Similarity:	95.46%	Conservative:	11
Best Local Similarity:	92.97%	Mismatches:	20
Query Match:	87.77%	Indels:	0
DB:	4	Gaps:	0

US-09-488-265B-30 (1-1404) x US-09-634-493A-1 (1-441)

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Qy        79 AACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCAC 138
Db         1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20

Qy       139 TTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGAC 198
Db        21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40

Qy       199 GTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATAC 258
Db        41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60

Qy       259 CCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCT 318
Db        61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80

Qy       319 ACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
Db        81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

Qy       379 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGA 438
Db       101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120

Qy       439 TACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTT 498
Db       121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140

Qy       499 ATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGT 558
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Db        141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160

Qy        559 GCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTAC 618
              :::  |||||||||||:|||||||||||:::|||||||||||||||||||:::|:||||
Db        161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180

Qy        619 AACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGAC 678
              ||||||||||||||||||||  ||||||||||||||:::|||||||||||||||||||.
Db        181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

Qy        679 GTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCAC 738
              ||||||||||||||||||||:::|:||||||||  ||||||||||||||||||||
Db        201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220

Qy        739 TTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTC 798
              ||||||||||||  ||||:|||||||||||||||  ||||||||||||||||||||||
Db        221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240

Qy        799 GACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACT 858
              :::|||||||||||||||||||||||||||:::|||||||||||||||  ||||||||||
Db        241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260

Qy        859 CACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGT 918
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280

Qy        919 GCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGA 978
              ||||||||||||||||||||||||||||||||||||  ||||||||||||.|||.|
Db        281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

Qy        979 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCA 1038
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320

Qy       1039 GCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTT 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db        321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340

Qy       1099 TCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTT 1158
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||.|||
Db        341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360

Qy       1159 GAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGA 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380

Qy       1219 GCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||:|||||
Db        381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

Qy       1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGA 1338
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420

Qy       1339 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTC 1398
              ||||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db        421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440

Qy       1399 GCT 1401
              |||
Db        441 Ala 441

RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2

Alignment Scores:
Pred. No.:                2.69e-204       Length:          467
Score:                    2170.00         Matches:         416
Percent Similarity:       87.68%          Conservative:    11
Best Local Similarity:    85.42%          Mismatches:      20
Query Match:              87.29%          Indels:          40
DB:                       3               Gaps:            2

US-09-488-265B-30 (1-1404) x US-09-121-425-2 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              ||||||||||||||||||||||||  ||||||||:::|||||||  ||||||
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||  ||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla--------- 97

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
                                                                ||||||||
Db         98 ----------------------------------------------------ThrTyrAsn 100

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC--------- 591
              ||||||||||||||||||:::  |||||||||||||||||||||||:::
Db        161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

Qy        592 ----------------------------------------------------GTTATTATT 600
                                                                  |||||||||
Db        181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              |||||||||:::|||||||||||||||||||||||||||  ||||||||||||||:::
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              ||||||||||||||||||||||||||||||||||||||:::|||||||||  ||||||
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
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Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-2
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Alignment Scores:
Pred. No.:              2.69e-204       Length:         467
Score:                  2170.00         Matches:        416
Percent Similarity:     87.68%          Conservative:   11
Best Local Similarity:  85.42%          Mismatches:     20
Query Match:            87.29%          Indels:         40
DB:                     4               Gaps:           2

US-09-488-265B-30 (1-1404) x US-09-634-493A-2 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla--------- 97

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db         98 ----------------------------------------------------ThrTyrAsn 100

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC--------- 591
Db        161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

Qy        592 ----------------------------------------------------GTTATTATT 600
Db        181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
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Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||| |||||||||||| |||| |||||||||||||| ||||| |||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              |||||||||||||||||||||||    |||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||:::|||||||||||||||||||||||||||||||||||   |||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||   ||||||||||||||||||||||||||||:::|||||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||    |||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
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Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 6
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
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;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33

Alignment Scores:
Pred. No.:                1.29e-176      Length:          465
Score:                    1888.00        Matches:         359
Percent Similarity:       84.37%         Conservative:    35
Best Local Similarity:    76.87%         Mismatches:      71
Query Match:              75.95%         Indels:          2
DB:                       3              Gaps:            2

US-09-488-265B-30 (1-1404) x US-08-868-435-33 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||             |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              |||     ||||||||||||||   ||||||||||||||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              :::::::|||      :::||||||   ||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              |||||||||||||||||||||||||||||   ||||||   |||      |||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   |||||||||   ||||||||||:::|||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              |||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||||||||||||||||   :::|||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
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Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||      ::::::||:::|||   |||:::'||||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||         :::|||||||||||||||||||||:::||||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||:::|||||||||:::|||   |||||||||||||||:::||||||||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   ||   |||||||||||||||   |||||||||||||||:||||||:::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   |||||||||||||||||||||||||||||:::||||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   ||||||||||||:::|||||   :::|||:::||:|||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   |||||||||||||:|||||||||||||||||:::|||   ||:||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||||||||||||||||||||||||||||||||:||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||||||||||||   :::|||   ||||||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||   ||||||||||||   |||   ||||||||||:::::||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||   |||:::||'||||||||||||||||||||||||||   ||||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||   :::||||||||||:::||||||||||:::||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
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Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 7
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33

Alignment Scores:
Pred. No.:                1.29e-176      Length:          465
Score:                    1888.00        Matches:         359
Percent Similarity:       84.37%         Conservative:    35
Best Local Similarity:    76.87%         Mismatches:      71
Query Match:              75.95%         Indels:          2
DB:                       4              Gaps:            2

US-09-488-265B-30 (1-1404) x US-08-744-231-33 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||               |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
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Qy        61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db        21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy       121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db        40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59

Qy       181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db        60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy       241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db        80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy       301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db       100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy       361 TACACTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db       120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy       421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db       140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy       481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db       160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy       541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTACT 600
Db       180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy       601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db       199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy       661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db       219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy       721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db       239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy       781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db       259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy       841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db       279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy       901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db       299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheThr 318

Qy       961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db       319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy      1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db       339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy      1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db       359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy      1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db       379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy      1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db       399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy      1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db       419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy      1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db       439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy      1381 AACTGGGAAGAATGTTTCGCT 1401
Db       459 AsnTrpGlyGluCysPheSer 465
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RESULT 6
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-78

Alignment Scores:

Pred. No.:	1.29e-176	Length:	465
Score:	1888.00	Matches:	359
Percent Similarity:	84.37%	Conservative:	35
Best Local Similarity:	76.87%	Mismatches:	71
Query Match:	75.95%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-30 (1-1404) x US-09-044-718-78 (1-465)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99
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Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTACAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465
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RESULT 9
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/09/636,499
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Alignment Scores:

Pred. No.:	1.29e-176	Length:	465
Score:	1888.00	Matches:	359
Percent Similarity:	84.37%	Conservative:	35
Best Local Similarity:	76.87%	Mismatches:	71
Query Match:	75.95%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-30 (1-1404) x US-09-636-499-6 (1-465)

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Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
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Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
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Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 10
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
;  APPLICANT:  Svendsen, Allan
;  TITLE OF INVENTION:  Phytase Variants
;  FILE REFERENCE:  5618.500-US
;  CURRENT APPLICATION NUMBER: US/09/273,871A
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER:  PA 1998 00407
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  PA 1998 00806
;  PRIOR FILING DATE:  1998-06-19
;  PRIOR APPLICATION NUMBER:  PA 1998 01176
;  PRIOR FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  PA 1999 00091
;  PRIOR FILING DATE:  1999-01-22
;  PRIOR APPLICATION NUMBER:  60/080,129
;  PRIOR FILING DATE:  1998-03-31
;  PRIOR APPLICATION NUMBER:  60/090,675
;  PRIOR FILING DATE:  1998-06-25
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-273-871A-8

Alignment Scores:
Pred. No.:                1.29e-176      Length:          465
Score:                    1888.00        Matches:         359
Percent Similarity:       84.37%         Conservative:    35
Best Local Similarity:    76.87%         Mismatches:      71
Query Match:              75.95%         Indels:          2
DB:                       4              Gaps:            2

US-09-488-265B-30 (1-1404) x US-09-273-871A-8 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
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Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   |||   ||||||||||||||||   ||||||||||||||||||||||:::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   ||||||||||||||||||||||||||||||:::|||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   ||||||||||||:::|||||   :::|||:::||||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||,||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||,|||||   ||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   ||||||||||||||||||||||||||||||||:::|||   ||||||.|||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              ||||||||||:::|||||||||||||||||||||||||||||||||||||||:|||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   |||:||||||||||   :::|||   ||||||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||   |||||||||:||   |||   |||||||||:::::|||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||   |||:::|||||||||||||||||||||||||||||||   ||||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||   :::|||||||||:::|||:|||||:::|||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   ||||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 11
US-09-044-718-80
; Sequence 80, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus

US-09-044-718-80

Alignment Scores:
Pred. No.:              7.87e-176     Length:          465
Score:                  1880.00       Matches:         358
Percent Similarity:     84.15%        Conservative:    35
Best Local Similarity:  76.66%        Mismatches:      72
Query Match:            75.62%        Indels:          2
DB:                     4             Gaps:            2

US-09-488-265B-30 (1-1404) x US-09-044-718-80 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||                 |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||             |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              |||      ||||||||||||||   ||||||||||||||||||||   |||||.
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ::::::|||      :::||||||   |||||.:::|||   ||||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              |||||||||||||||||||||||||||||   ||||||   |||      |||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||||   ||||||||   ||||:||||||||:::|||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              |||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||||||||||||||||.|||   :::|||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||      ::::::|||:::|||   |||:::||||||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||         :::||||||||||||||||||||:::||||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||:::||||||||:::|||   ||||||||||||||:::|||||||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   |||   ||||||||||||||   ||||||||||||||||||||:::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   ||||||||||||||||||||||||||||||:::|||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   ||||||||||||:::|||||   :::|||:::||||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
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Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   ||||||||||||||||||||||||||||||||:::|||   ||||||:||
Db        339 ThrLeuValSerAsnProAlaThrProProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||||||.||||||||||||||||||||||||||||||||:::||||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||||||||||||||   :::|||   ||:|||||||:|||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              ||||||||   ||:|||:|||||   |||   |||||||||::::::|:|||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||   |||:::||||||||||||||||||||||||||||||   ||||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              |||||||||||||||   :::|||||||||:::|||||||||:::||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   ||||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 12
US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-79

Alignment Scores:
Pred. No.:              9.86e-176       Length:         465
Score:                  1879.00         Matches:        358
Percent Similarity:     84.15%          Conservative:   35
Best Local Similarity:  76.66%          Mismatches:     72
Query Match:            75.58%          Indels:         2
DB:                     4               Gaps:           2

US-09-488-265B-30 (1-1404) x US-09-044-718-79 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||                |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||            |||   |||   ||||||||||||||||   ||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              |||      ||||||||||||||   ||||||||||||||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              :::::::|||      :::|||||||   ||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||||||||||   ||||||   |||      |||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   ||||||||   ||||||||||||:::||||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||:|||||||||||||   :::||||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||   |||||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||||      :::::::|||:::|||   |||:::||||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||         :::||||||||||||||||||:::||||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||:::||||||||||:::|||   ||||||||||||||||:::||||||||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   |||   ||||||||||||||   ||||||||||||||||||||:::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   ||||||||||||||||||||||||||||||:::||||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAAATCTTTGGGT 900
              ||||||   ||||||||||||:::||||||   :::|||:::||||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   ||||||||||||||||||||||||||||||||:::|||   ||||||:||
Db        339 ThrLeuValSerAsnProAlaThrProProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||||||.||||||||||||||||||||||||||||||||:::||||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378
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Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
             ||||||   ||||||||||||||||   :::|||   |||||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
             |||||||||   ||||||||||||   |||   |||||||||:::::|||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
             |||||||||   |||:::|||||||||||||||||||||||||||||   ||||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
             ||||||||||||||||   :::|||||||||||:::|||||||||:::||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
             ||||||   |||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 13
US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Alignment Scores:
Pred. No.:              1.07e-175       Length:         439
Score:                  1878.50         Matches:        351
Percent Similarity:     87.73%          Conservative:   35
Best Local Similarity:  79.77%          Mismatches:     53
Query Match:            75.56%          Indels:         1
DB:                     4               Gaps:           1

US-09-488-265B-30 (1-1404) x US-09-044-718-3 (1-439)

Qy         82 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 141
              |||   ||||||||||||||||||   ||||||||||   |||      |||||||:|
Db          1 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 20

Qy        142 TGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGTT 201
              ||||||   ||||||||||||||||||   |||||   ::::::|||      :::
Db         21 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 40

Qy        202 CCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 261
              ||||||   |||||:::|||   ||||||||||||||||||||||||||||||||||||
Db         41 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 60

Qy        262 ACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 321
              |||||||||   ||||||   |||      |||:::   |||||||||   |||||||||
Db         61 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 80

Qy        322 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 381
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||||

Db         81 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 100

Qy        382 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 441
              |||||||||||||||||||||||||:::|||||||||||||||||||||||:::||||||
Db        101 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 120

Qy        442 AAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTATT 501
              ||||||||||||||||   :::|||||||||||||||||||||||||||||||||||||
Db        121 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 140

Qy        502 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTGCT 561
              ||||||   ||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        141 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 160

Qy        562 AACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAAC 621
                  :::::::|||:::|||   |||:::|||||||||||||||          :::|||
Db        161 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 179

Qy        622 AACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTT 681
              |||||||||||||||||:::||||||   ||||||   |||:::|||||||||:::|||
Db        180 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 199

Qy        682 GAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTG 741
              ||||||||||||||:::|||||||||   ||||||||||   |||   |||||
Db        200 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 219

Qy        742 CCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGAC 801
              |||||||||   |||||||||||||||||||||:::|||||||||||||||   ||||||
Db        220 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 239

Qy        802 ACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACTCAC 861
              |||||||||||||||||||:|||||:::|||||||||:|||||||   ||||||||||:
Db        240 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 259

Qy        862 GACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCT 921
              :::||||||   :::|||:::|||||||||||||||||||:|||||||||||||||||||
Db        260 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 279

Qy        922 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTG 981
              |||||||||||||||||||||||||||:::|||||   |||||||||||||||||||||
Db        280 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 299

Qy        982 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1041
              |||   |||||||||||||||||||||||||||||   ||||||   ||||||||||||
Db        300 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 319

Qy       1042 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTCT 1101
              |||||||:|||||||||||||:::|||   |||||||||||||||||:::|||||||||
Db        320 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 339

Qy       1102 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTTGAA 1161
              |||||||||||||||||||||||||||||||:::|||||||   ||||||||||||||
Db        340 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 359

Qy       1162 TCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1221
              |||   :::|||   |||||||||||||||||||||   ||||||||   ||||||||
Db        360 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 379

Qy       1222 TACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1281
              |||   |||   |||||||||:::::|||||||||||||||||||||||   ||:::|||
Db        380 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 399

Qy       1282 GACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1341
              |||||||||||||||||||||||||||||||   |||||||||||||||||||||||   :::
Db        400 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 419

Qy       1342 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGCT 1401
              |||||||||:::|||||||||:::|||||||||||||||||||||||||   ||||||||||:::
Db        420 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 439

RESULT 14
US-09-044-718-12
; Sequence 12, Application US/09044718
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; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Alignment Scores:
Pred. No.:              1.08e-175     Length:          449
Score:                  1878.50       Matches:         351
Percent Similarity:     87.73%        Conservative:    35
Best Local Similarity:  79.77%        Mismatches:      53
Query Match:            75.56%        Indels:          1
DB:                     4             Gaps:            1

US-09-488-265B-30 (1-1404) x US-09-044-718-12 (1-449)

Qy        82 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 141
Db        11 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 30

Qy       142 TGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGTT 201
Db        31 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 50

Qy       202 CCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 261
Db        51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70

Qy       262 ACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 321
Db        71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90

Qy       322 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 381
Db        91 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110

Qy       382 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 441
Db       111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130

Qy       442 AAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTICTGGTTCTGACAGAGTTATT 501
Db       131 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 150

Qy       502 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTGCT 561
Db       151 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 170

Qy       562 AACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAAC 621
Db       171 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189

Qy       622 AACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTT 681
Db       190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209

Qy       682 GAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTG 741
Db       210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 229

Qy       742 CCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGAC 801
Db       230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249

Qy       802 ACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACTCAC 861
Db       250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269

Qy       862 GACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCT 921
Db       270 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 289

Qy       922 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTG 981
Db       290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309

Qy       982 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1041
Db       310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329

Qy      1042 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTCT 1101
Db       330 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 349

Qy      1102 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTTGAA 1161
Db       350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 369

Qy      1162 TCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1221
Db       370 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 389

Qy      1222 TACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1281
Db       390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409

Qy      1282 GACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1341
Db       410 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 429

Qy      1342 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGCT 1401
Db       430 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 449

RESULT 15
US-09-044-718-81
; Sequence 81, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Alignment Scores:
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Pred. No.:	1.94e-175	Length:	465
Score:	1876.00	Matches:	357
Percent Similarity:	84.15%	Conservative:	36
Best Local Similarity:	76.45%	Mismatches:	72
Query Match:	75.46%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-30 (1-1404) x US-09-044-718-81 (1-465)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||                 ||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
                 |||      ||||||||||||||||   ||||||||||||||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
                 ::::::|||      :::||||||   ||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              |||||||||||||||||||||||||||||||,   ||||||   |||   |||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   ||||!||||   ||||||||||||:::||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              |||||||||||||||||.||||:||||   ||||||||||||||:::||||:||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrAlaPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::||||||||||||||||||||   :::||||||||||||:|:|||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||||||||||||||||||||   ||||||||||||||||||||||   ||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||      ::::::||:::::|||   |||:::|,|||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||         :::|||||,|||||||||||||||:::|||:'|   |||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||:::|||||||||:::|||   |||||||||||||||:::|:|||||'|   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   :::   |||||||||||||||   ||||||||||||||||||||:::|||
Db        239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   |||||||||||||||||||||||||||:::||||||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   ||||||||||||:::||||||   :::|||:::||||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||,
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||!|,||||||||||||||||   ||||||||||,||||||||||||,||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   ||||||||||||||||||||||||||||||||:::|||   |||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||||||||||||   :::|||   ||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              ||||||||   ||||||||||||   |||   ||||||||:::::|||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              ||||||||   ||:::|||||||||||||||||||||||||,||||   ||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   :::|||||||:::|||||||:::|||||||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   ||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465
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GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

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(without alignments)
6289.894 Million cell updates/sec

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Perfect score: 2480
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 1175308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2408	97.1	467	14	US-10-083-452-9	Sequence 9, Appli
2	1875	75.6	467	15	US-10-079-709-32	Sequence 32, Appl
3	1875	75.6	467	15	US-10-229-358-5	Sequence 5, Appli
4	1867	75.3	465	14	US-10-083-452-8	Sequence 8, Appli
5	1867	75.3	465	15	US-10-062-848-78	Sequence 78, Appl
6	1867	75.3	465	15	US-10-229-358-6	Sequence 6, Appli
7	1863	75.1	467	14	US-10-083-452-11	Sequence 11, Appl
8	1860.5	75.0	474	15	US-10-213-990-24	Sequence 24, Appl
9	1860	75.0	467	9	US-09-929-060-3	Sequence 3, Appli
10	1859	75.0	465	15	US-10-062-848-80	Sequence 80, Appl
11	1858	74.9	465	15	US-10-062-848-79	Sequence 79, Appl
12	1857.5	74.9	439	15	US-10-062-848-3	Sequence 3, Appli
13	1857.5	74.9	449	15	US-10-062-848-12	Sequence 12, Appl
14	1855	74.8	465	15	US-10-062-848-81	Sequence 81, Appl
15	1851	74.6	462	15	US-10-229-358-12	Sequence 12, Appl
16	1845	74.4	469	15	US-10-062-848-82	Sequence 82, Appl
17	1835.5	74.0	463	14	US-10-083-452-10	Sequence 10, Appl
18	1833	73.9	444	15	US-10-062-848-1	Sequence 1, Appli
19	1820.5	73.4	447	15	US-10-062-848-6	Sequence 6, Appli
20	1818	73.3	443	9	US-09-929-060-1	Sequence 1, Appli
21	1813	73.1	443	9	US-09-929-060-2	Sequence 2, Appli
22	1765	71.2	450	15	US-10-062-848-15	Sequence 15, Appl
23	1761	71.0	466	14	US-10-083-452-12	Sequence 12, Appl
24	1761	71.0	466	15	US-10-229-358-7	Sequence 7, Appli
25	1719	69.3	466	14	US-10-083-452-13	Sequence 13, Appl
26	1715.5	69.2	450	15	US-10-062-848-9	Sequence 9, Appli
27	1714	69.1	438	15	US-10-062-848-2	Sequence 2, Appli
28	1627	65.6	489	15	US-10-229-358-4	Sequence 4, Appli
29	1627	65.6	489	15	US-10-229-358-10	Sequence 10, Appl
30	1613	65.0	410	15	US-10-229-358-11	Sequence 11, Appl
31	1334	53.8	475	14	US-10-083-452-14	Sequence 14, Appl
32	1313.5	53.0	487	14	US-10-083-452-15	Sequence 15, Appl
33	1313.5	53.0	487	15	US-10-229-358-8	Sequence 8, Appli
34	1311	52.9	355	15	US-10-229-358-15	Sequence 15, Appl
35	1187	47.9	495	14	US-10-083-452-2	Sequence 2, Appli
36	1182	47.7	478	14	US-10-083-452-3	Sequence 3, Appli
37	902	36.4	284	15	US-10-229-358-19	Sequence 19, Appl
38	855	34.5	283	15	US-10-229-358-9	Sequence 9, Appli
39	855	34.5	283	15	US-10-229-358-24	Sequence 24, Appl
40	802.5	32.4	443	14	US-10-083-452-5	Sequence 5, Appli
41	798.5	32.2	439	14	US-10-083-452-7	Sequence 7, Appli
42	795.5	32.1	453	14	US-10-083-452-6	Sequence 6, Appli
43	781	31.5	442	14	US-10-083-452-4	Sequence 4, Appli
44	702.5	28.3	212	15	US-10-229-358-16	Sequence 16, Appl
45	401	16.2	312	15	US-10-229-358-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25

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;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Variation
US-10-083-452-9

Alignment Scores:
Pred. No.:              2.77e-198       Length:         467
Score:                  2408.00         Matches:        457
Percent Similarity:     98.50%          Conservative:   3
Best Local Similarity:  97.86%          Mismatches:     7
Query Match:            97.10%          Indels:         0
DB:                     14              Gaps:           0

US-09-488-265B-28 (1-1404) x US-10-083-452-9 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
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Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGln 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
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Db        101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
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Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
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Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
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Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
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Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
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Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
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Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
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RESULT 2
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/079,709
;      FILING DATE:  02-FEB-2002
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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/233,510
;      FILING DATE:  20-JAN-1999
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-079-709-32

Alignment Scores:
Pred. No.:              1.84e-152      Length:          467
Score:                  1875.00        Matches:         353
Percent Similarity:     84.37%         Conservative:    41
Best Local Similarity:  75.59%         Mismatches:      73
Query Match:            75.60%         Indels:          0
DB:                     15             Gaps:            0

US-09-488-265B-28 (1-1404) x US-10-079-709-32 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
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Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||:::          |||      ||||||||||||||||||   |||||||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||  |||||||:|||||||  |||:::|||:::|||||||||||:::|||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||   |||||||||:::|:|||||      |||||||||||||||   |||||:|||||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              |||||||||||||||||||||||||  |||      |||  ||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
                ||||||:::|||||||||  |||  ||||||||||||||||||||||:|||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||:::|||||||:|||||||||||||||||||||||||   :::::|||||||||||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||:::::|||   |||  |||||||||||||||||:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
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Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||   ||||||   :::||||||   |||:::||||||   |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
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Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

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              |||||||||   |||  |||||||||||||||||||||||   |||   ||:::|||||||
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
                 |||||||||   ||||||   ||||||||||||||||||   :::|||   ||||||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||   |||||||||::::::   ::::::      |||:::|||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||:::|||||||||||||||||||||||||   |||:|||||||:::|||
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||||||   |||   |||||||:||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||:::|||||||||||||||||||||||:::|||||||||||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              |||||||||   :::|||||||||   |||||||||:|||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||:::|||||:::|||   :::|||||||||:::|||:::::|||||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              ||||||||||||:::|||   |||||||||||||||||||||||||||:::|||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   ||||||   ||||||   ||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              :::|||||||||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 3
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Sam
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 467
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; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-229-358-5

Alignment Scores:

Pred. No.:	1.84e-152	Length:	467
Score:	1875.00	Matches:	353
Percent Similarity:	84.37%	Conservative:	41
Best Local Similarity:	75.59%	Mismatches:	73
Query Match:	75.60%	Indels:	0
DB:	15	Gaps:	0

US-09-488-265B-28 (1-1404) x US-10-229-358-5 (1-467)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||||||||      |||||||||   :::      |||   |||   |||||||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||:::          |||      ||||||||||||||||||   ||||.||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||   ||||||||||||||||   |||:::|||:::||||||||||:::|||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||   |||||||||:::|||||      |||||||||||||   |||||||||:|||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              |||||||||||||||||||||   |||      |||   |||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||:::|||||||||   |||   ||||||||||||||||||||||||||||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||:::||||||||||||||||||||||||||||||||   ::::::||||||||||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::||||||:::::|||   |||   ||||||||||||||||||:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||   ||||||||||||||   :::||||||||||||||||||||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||   ||||||   :::||||||   |||:::||||||   |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
              |||   |||      ||||||||||||||   ||||||||||   |||||||||
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||||||||   |||   ||||||||||||||||||||   |||   |||:::||||||
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              |||||||||   ||||||   ||||||||||||||||||   :::|||   ||||||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||   ||||||||||::::::   ::::::      |||:::||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   ||||||||||||||||||||||||   ||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||:::|||||||||||||||||||||||||||   ||||||||||||:::|||
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||||||||||   |||   ||||||:::||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||:::|||||||||||||||||||||||||:::|||||||||||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              |||||||||   :::|||||||||   ||||||||||||||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||:::|||||:::|||   :::|||||||||:::|||:::::|||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              |||||||||||||:::|||   ||||||||||||||||||||||||||||:::||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              |||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   ||:|||   ||||||   ||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              :::|||||||||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467
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RESULT 4
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

Alignment Scores:

Pred. No.:	8.97e-152	Length:	465
Score:	1867.00	Matches:	355
Percent Similarity:	83.73%	Conservative:	36

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Best Local Similarity:  76.02%          Mismatches:     74
Query Match:            75.28%          Indels:         2
DB:                     14              Gaps:           2

US-09-488-265B-28 (1-1404) x US-10-083-452-8 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||               |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
                 |||      ||||||||||||||||   |||||||||:::|||||||||   :||||.
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
                 ::::::|||      :::|||   ||||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||   ||||||   |||      ||||::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   |||||||||   ||||||||||||:::|||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||   |||:::||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||:::|||||||||||||||||||   :::||||||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||   |||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||||||||||||:::      ::::::|||::|||   |||:::|||||||||
Db        180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
              ||||||         :::|:|:||||||||||||||||||   ||||||   |||||.
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||:::|||||||||||:::|||   |||||||||||||||||||||||!!   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              ||||||   |||      |.||||||||||||||||||||||||||||||||||   |||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||   |||||||||||||||||||||||||||||:::::|||||||:
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   ||||||||||||:::||||||   :::|||:::|||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   |||||:||||||||:|||||||||||||:::|||   |||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              ||||||||||:::|| :::|||||||||||||||||||||||||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||||||||||||||   :::|||   ||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              |||||||||   ||||||||||||   |||   |||||||||:::::|||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              |||||||||||||||   :::||||||||||:::|||||||:::|||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              |||||||||||||||   :::||||||||||:::|||||||:::|||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              ||||||   ||||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 5
US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-78

Alignment Scores:
Pred. No.:              8.97e-152       Length:         465
Score:                  1867.00         Matches:        355
Percent Similarity:     83.73%          Conservative:   36
Best Local Similarity:  76.02%          Mismatches:     74
Query Match:            75.28%          Indels:         2
DB:                     15              Gaps:           2

US-09-488-265B-28 (1-1404) x US-10-062-848-78 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||               |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
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Qy       121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
Db        40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy       181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db        60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy       241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
Db        80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99

Qy       301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db       100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy       361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
Db       120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy       421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db       140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy       481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db       160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy       541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
Db       180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198

Qy       601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db       199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy       661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db       219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy       721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db       239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy       781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db       259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy       841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db       279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy       901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db       299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy       961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db       319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy      1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db       339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy      1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db       359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy      1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db       379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy      1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db       399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy      1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db       419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy      1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db       439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy      1381 AACTGGGCTGAATGTTTCGCT 1401
Db       459 AsnTrpGlyGluCysPheSer 465
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RESULT 6
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Alignment Scores:

Pred. No.:	8.97e-152	Length:	465
Score:	1867.00	Matches:	355
Percent Similarity:	83.73%	Conservative:	36
Best Local Similarity:	76.02%	Mismatches:	74
Query Match:	75.28%	Indels:	2
DB:	15	Gaps:	2

US-09-488-265B-28 (1-1404) x US-10-229-358-6 (1-465)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
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Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
Db        180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 7
US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
;  APPLICANT: Svendsen, Allan
;  TITLE OF INVENTION: Phytase Variants
;  FILE REFERENCE: 5618.500-US
;  CURRENT APPLICATION NUMBER: US/10/083,452
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: US/09/273,871
;  PRIOR FILING DATE: 1999-03-22
;  PRIOR APPLICATION NUMBER: PA 1998 00407
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: PA 1998 00806
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: PA 1998 01176
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: PA 1999 00091
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/080,129
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/090,675
;  PRIOR FILING DATE: 1998-06-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus ficuum
US-10-083-452-11

Alignment Scores:
Pred. No.:                1.98e-151      Length:          467
Score:                    1863.00        Matches:         351
Percent Similarity:       83.94%         Conservative:    41
Best Local Similarity:    75.16%         Mismatches:      75
Query Match:              75.12%         Indels:          0
DB:                       14             Gaps:            0

US-09-488-265B-28 (1-1404) x US-10-083-452-11 (1-467)

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Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCCATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
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Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuLysSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnAlaPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 8
US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Bo
;  APPLICANT:  Bussey, Howard
;  APPLICANT:  Storms, Reg
;  APPLICANT:  Roemer, Terry
;  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
;  TITLE OF INVENTION:  ENZYMES AND METHODS OF USE
;  FILE REFERENCE: 10182-019-999
;  CURRENT APPLICATION NUMBER: US/10/213,990
;  CURRENT FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Aspergillus
US-10-213-990-24

Alignment Scores:
Pred. No.:              3.27e-151       Length:         474
Score:                  1860.50         Matches:        351
Percent Similarity:     84.12%          Conservative:   41
Best Local Similarity:  75.32%          Mismatches:     67
Query Match:            75.02%          Indels:         7
Db:                     15              Gaps:           2

US-09-488-265B-28 (1-1404) x US-10-213-990-24 (1-474)

Qy          4 GGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACCGCC 63
Db         16 GlyAlaValValLeuIleLeuLysArgSerArgValSerAlaAlaProSerSer------ 33

Qy         64 TTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTC 123
Db         34 ----------AlaGlySerLysSerCysAspThrValAspLeuGlyTyrGlnCysSer 49

Qy        124 CCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAATCT 183
Db         50 ProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeu 69

Qy        184 GCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGA 243
Db         70 SerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSerArg 89

Qy        244 CACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAAGCT 303
Db         90 HisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThrAla 109

Qy        304 ATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTAC 363
Db        110 IleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyr 129

Qy        364 ACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGTATT 423
Db        130 ThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIle 149

Qy        424 AAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCT 483
Db        150 LysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAlaSer 169

Qy        484 GGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAG 543
Db        170 GlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLys 189

Qy        544 TTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATTCCA 603
Db        190 LeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIlePro 208

Qy        604 GAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGACTCT 663
Db        209 GluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAlaSer 228

Qy        664 GAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGAGCT 723
Db        229 GlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAla 248

Qy        724 AGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTGATG 783
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(without alignments)
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265_@CGN_1_1_99_@runat_03102003_074813_12239 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2308	92.8	467	4	US-09-273-871A-9	Sequence 9, Appli
2	2182	87.8	441	3	US-09-121-425-1	Sequence 1, Appli
3	2182	87.8	441	4	US-09-634-493A-1	Sequence 1, Appli
4	2170	87.3	467	3	US-09-121-425-2	Sequence 2, Appli
5	2170	87.3	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1888	75.9	465	3	US-08-868-435-33	Sequence 33, Appl
7	1888	75.9	465	4	US-08-744-231-33	Sequence 33, Appl
8	1888	75.9	465	4	US-09-044-718-78	Sequence 78, Appl
9	1888	75.9	465	4	US-09-636-499-6	Sequence 6, Appli
10	1888	75.9	465	4	US-09-273-871A-8	Sequence 8, Appli
11	1880	75.6	465	4	US-09-044-718-80	Sequence 80, Appl
12	1879	75.6	465	4	US-09-044-718-79	Sequence 79, Appl
13	1878.5	75.6	439	4	US-09-044-718-3	Sequence 3, Appli
14	1878.5	75.6	449	4	US-09-044-718-12	Sequence 12, Appl
15	1876	75.5	465	4	US-09-044-718-81	Sequence 81, Appl
16	1854	74.6	469	4	US-09-044-718-82	Sequence 82, Appl
17	1852	74.5	467	1	US-07-923-724-8	Sequence 8, Appli
18	1852	74.5	467	2	US-08-609-426A-8	Sequence 8, Appli
19	1852	74.5	467	2	US-08-374-652C-2	Sequence 2, Appli
20	1848	74.3	467	1	US-08-151-574-32	Sequence 32, Appl
21	1848	74.3	467	1	US-08-146-424-20	Sequence 20, Appl
22	1848	74.3	467	1	US-08-693-709-2	Sequence 2, Appli
23	1848	74.3	467	2	US-08-419-448-32	Sequence 32, Appl
24	1848	74.3	467	2	US-08-819-825-3	Sequence 3, Appli
25	1848	74.3	467	3	US-09-163-642-3	Sequence 3, Appli
26	1848	74.3	467	4	US-09-233-510-32	Sequence 32, Appl
27	1848	74.3	467	4	US-09-636-499-5	Sequence 5, Appli
28	1841	74.1	467	3	US-09-155-855-3	Sequence 3, Appli
29	1841	74.1	467	4	US-09-543-744-3	Sequence 3, Appli
30	1841	74.1	467	4	US-09-929-060-3	Sequence 3, Appli
31	1836	73.9	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1829	73.6	462	4	US-09-636-499-12	Sequence 12, Appl
33	1822	73.3	466	3	US-08-868-435-35	Sequence 35, Appl
34	1822	73.3	466	4	US-08-744-231-35	Sequence 35, Appl
35	1819	73.2	466	3	US-08-868-435-12	Sequence 12, Appl
36	1819	73.2	466	4	US-08-744-231-12	Sequence 12, Appl
37	1806	72.6	444	4	US-09-044-718-1	Sequence 1, Appli
38	1804.5	72.6	463	3	US-08-868-435-29	Sequence 29, Appl
39	1804.5	72.6	463	4	US-08-744-231-29	Sequence 29, Appl
40	1804.5	72.6	463	4	US-09-273-871A-10	Sequence 10, Appl
41	1799	72.4	443	3	US-09-155-855-1	Sequence 1, Appli
42	1799	72.4	443	4	US-09-543-744-1	Sequence 1, Appli
43	1799	72.4	443	4	US-09-929-060-1	Sequence 1, Appli
44	1794	72.2	443	3	US-09-155-855-2	Sequence 2, Appli
45	1794	72.2	443	4	US-09-543-744-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Alignment Scores:
Pred. No.: 7.66e-218 Length: 467
Score: 2308.00 Matches: 436
Percent Similarity: 95.72% Conservative: 11

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Best Local Similarity:  93.36%        Mismatches:    20
Query Match:            92.84%        Indels:        0
DB:                     4             Gaps:          0

US-09-488-265B-30 (1-1404) x US-09-273-871A-9 (1-467)

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Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
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Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              |||||||||||||||||||||
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

Alignment Scores:
Pred. No.:              1.73e-205     Length:        441
Score:                  2182.00       Matches:       410
Percent Similarity:     95.46%        Conservative:  11
Best Local Similarity:  92.97%        Mismatches:    20
Query Match:            87.77%        Indels:        0
DB:                     3             Gaps:          0

US-09-488-265B-30 (1-1404) x US-09-121-425-1 (1-441)

Qy         79 AACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCAC 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20

Qy        139 TTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGAC 198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40

Qy        199 GTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATAC 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60
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Qy       259 CCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCT 318
Db        61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80

Qy       319 ACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
Db        81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

Qy       379 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGA 438
Db       101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120

Qy       439 TACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTT 498
Db       121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140

Qy       499 ATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGT 558
Db       141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160

Qy       559 GCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTAC 618
Db       161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180

Qy       619 AACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGAC 678
Db       181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

Qy       679 GTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCAC 738
Db       201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220

Qy       739 TTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTC 798
Db       221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240

Qy       799 GACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACT 858
Db       241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260

Qy       859 CACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGT 918
Db       261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280

Qy       919 GCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGA 978
Db       281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

Qy       979 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCA 1038
Db       301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320

Qy      1039 GCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTT 1098
Db       321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340

Qy      1099 TCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTT 1158
Db       341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360

Qy      1159 GAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGA 1218
Db       361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380

Qy      1219 GCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
Db       381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

Qy      1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGA 1338
Db       401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420

Qy      1339 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTC 1398
Db       421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440

Qy      1399 GCT 1401
Db       441 Ala 441
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RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-1

Alignment Scores:

Pred. No.:	1.73e-205	Length:	441
Score:	2182.00	Matches:	410
Percent Similarity:	95.46%	Conservative:	11
Best Local Similarity:	92.97%	Mismatches:	20
Query Match:	87.77%	Indels:	0
DB:	4	Gaps:	0

US-09-488-265B-30 (1-1404) x US-09-634-493A-1 (1-441)

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Qy        79 AACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCAC 138
Db         1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20

Qy       139 TTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGAC 198
Db        21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40

Qy       199 GTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTGCTAGATAC 258
Db        41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60

Qy       259 CCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCT 318
Db        61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80

Qy       319 ACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
Db        81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

Qy       379 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGA 438
Db       101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120

Qy       439 TACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTT 498
Db       121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140

Qy       499 ATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGT 558
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Db        141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160

Qy        559 GCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTAC 618
              :::  |||||||||||||||||||||||||||||:::|||||||||||||||||||:::||| ||
Db        161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180

Qy        619 AACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGAC 678
              |||||||||||||||||||  |||||||||||||||:::|||||||||||||||||| ||
Db        181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

Qy        679 GTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCAC 738
              ||||||||||||||||||||||:::|||||||||  ||||||||||||||||||||
Db        201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220

Qy        739 TTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTC 798
              ||||||||||||  |||||||||||||||||||  |||||||||||||||||||||||
Db        221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240

Qy        799 GACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACT 858
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260

Qy        859 CACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGT 918
              ||||||||||||  |||||||||||||||||||||.|||||.|||||||||:|||:|||
Db        261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280

Qy        919 GCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGA 978
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

Qy        979 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCA 1038
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320

Qy       1039 GCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTT 1098
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db        321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340

Qy       1099 TCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTT 1158
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360

Qy       1159 GAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGA 1218
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380

Qy       1219 GCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

Qy       1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGA 1338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420

Qy       1339 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTC 1398
              ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db        421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440

Qy       1399 GCT 1401
              |||
Db        441 Ala 441
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```
RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2

Alignment Scores:
Pred. No.:                2.69e-204       Length:          467
Score:                    2170.00         Matches:         416
Percent Similarity:       87.68%          Conservative:    11
Best Local Similarity:    85.42%          Mismatches:      20
Query Match:              87.29%          Indels:          40
DB:                       3               Gaps:            2

US-09-488-265B-30 (1-1404) x US-09-121-425-2 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              ||||||||||||||||||||||||  |||||||||:::|||||||  ||||||
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla--------- 97

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
                                                                ||||||||||
Db         98 ----------------------------------------------------ThrTyrAsn 100

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db        101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC--------- 591
              ||||||||||||||||:::  |||||||||||||||||||||||||:::
Db        161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

Qy        592 ----------------------------------------------------GTTATTATT 600
                                                                  |||||||||
Db        181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              |||||||||:::|||||||||||||||||||||||||||||  ||||||||||||||:::
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||  ||||||
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
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Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TIILE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-2

Alignment Scores:
Pred. No.:                2.69e-204      Length:          467
Score:                    2170.00        Matches:         416
Percent Similarity:       87.68%         Conservative:    11
Best Local Similarity:    85.42%         Mismatches:      20
Query Match:              87.29%         Indels:          40
DB:                       4              Gaps:            2

US-09-488-265B-30 (1-1404) x US-09-634-493A-2 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla--------- 97

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db         98 ----------------------------------------------------ThrTyrAsn 100

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC--------- 591
Db        161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

Qy        592 ----------------------------------------GTTATTATT 600
Db        181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
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Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrProProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||:::|||||||||||||||||||||||||||||||||||   :||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||   ||||||||||||||||||||||||||||||:::|||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||.|||||||||||||||||   ||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||||||||||||||||||||||||.|||||||||||||||||||:||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   ||||||||||||
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 6
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363

;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33

Alignment Scores:
Pred. No.:                1.29e-176      Length:          465
Score:                    1888.00        Matches:         359
Percent Similarity:       84.37%         Conservative:    35
Best Local Similarity:    76.87%         Mismatches:      71
Query Match:              75.95%         Indels:          2
DB:                       3              Gaps:            2

US-09-488-265B-30 (1-1404) x US-08-868-435-33 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||                  |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              |||      ||||||||||||||   ||||:||||||||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              :::::::|||      :::||||||   ||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||   ||||||   |||      |||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   |||||||||   ||||||||||:::||||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::||||||||||||||||||||||   :::||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
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Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||   ||||||||||||.|||:||||||.   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||:      ::::::|||:::|||   |||:::|:|||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||         :::|||||||||||||||||||||||:::||||||   |||:|||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||:::|||||||||||:::|||   |||||||||||||||:::||||||,||   ||||:|
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   |||   |||||||||||||||,   |||||||||||||||||||||:::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   |||||||||||||||||||||||||||||||:::|||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   ||||||||||||:::|||||   :::|||:::|:|||||||||||||...
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              |||||:|||||||:|||||'|||||||||||||||||||||:|||:::||:'||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              |||||:|||||||||||:|||||   |||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   |||||||||:|||||'|||||||||||||||:::|||   ||'||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||||:||||:|||||||||||||||||||||||||||.:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||'|||||||||   :::|||   ||:|||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              ||||:|||||   |||||||'||||   |||   |||||.|||:::::::|||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||   |||:::|||||||||||||||||||||||||||||||   |||||||||:
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              |||||||||||||||   :::|||||||||||:::|||||||||||:::|||||||||||:
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   |||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 7
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
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;      LOCATION:  205
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;    FEATURE:
;      NAME/KEY:  misc_feature
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;    FEATURE:
;      NAME/KEY:  misc_feature
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;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33

Alignment Scores:
Pred. No.:                1.29e-176      Length:          465
Score:                    1888.00        Matches:         359
Percent Similarity:       84.37%         Conservative:    35
Best Local Similarity:    76.87%         Mismatches:      71
Query Match:              75.95%         Indels:          2
DB:                       4              Gaps:            2

US-09-488-265B-30 (1-1404) x US-08-744-231-33 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||               |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
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Qy        61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db        21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy       121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db        40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy       181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db        60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy       241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db        80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy       301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db       100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy       361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db       120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy       421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCAATCATTAGAGCT 480
Db       140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy       481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db       160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy       541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db       180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy       601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db       199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy       661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db       219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy       721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db       239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy       781 ATGGACATGTGTCCAATCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db       259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy       841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db       279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy       901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db       299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy       961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db       319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy      1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db       339 ThrLeuValSerAsnProAlaThrProProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy      1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db       359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy      1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db       379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy      1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db       399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy      1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db       419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy      1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db       439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy      1381 AACTGGGAAGAATGTTTCGCT 1401
Db       459 AsnTrpGlyGluCysPheSer 465
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RESULT 8
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-78

Alignment Scores:

Pred. No.:	1.29e-176	Length:	465
Score:	1888.00	Matches:	359
Percent Similarity:	84.37%	Conservative:	35
Best Local Similarity:	76.87%	Mismatches:	71
Query Match:	75.95%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-30 (1-1404) x US-09-044-718-78 (1-465)

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Qy         1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db         1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy        61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db        21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy       121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db        40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy       181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db        60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy       241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db        80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99
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Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465
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RESULT 9
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/09/636,499
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Alignment Scores:

Pred. No.:	1.29e-176	Length:	465
Score:	1888.00	Matches:	359
Percent Similarity:	84.37%	Conservative:	35
Best Local Similarity:	76.87%	Mismatches:	71
Query Match:	75.95%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-30 (1-1404) x US-09-636-499-6 (1-465)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
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Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        339 ThrLeuValSerAsnProAlaThrProProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 10
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
;  APPLICANT:  Svendsen, Allan
;  TITLE OF INVENTION:  Phytase Variants
;  FILE REFERENCE:  5618.500-US
;  CURRENT APPLICATION NUMBER: US/09/273,871A
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER:  PA 1998 00407
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  PA 1998 00806
;  PRIOR FILING DATE:  1998-06-19
;  PRIOR APPLICATION NUMBER:  PA 1998 01176
;  PRIOR FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  PA 1999 00091
;  PRIOR FILING DATE:  1999-01-22
;  PRIOR APPLICATION NUMBER:  60/080,129
;  PRIOR FILING DATE:  1998-03-31
;  PRIOR APPLICATION NUMBER:  60/090,675
;  PRIOR FILING DATE:  1998-06-25
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-273-871A-8

Alignment Scores:
Pred. No.:                1.29e-176      Length:          465
Score:                    1888.00        Matches:         359
Percent Similarity:       84.37%         Conservative:    35
Best Local Similarity:    76.87%         Mismatches:      71
Query Match:              75.95%         Indels:          2
DB:                       4              Gaps:            2

US-09-488-265B-30 (1-1404) x US-09-273-871A-8 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
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Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780

Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840

Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900

Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960

Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020

Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080

Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140

Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200

Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260

Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320

Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380

Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401

Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 11
US-09-044-718-80
; Sequence 80, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus

US-09-044-718-80

Alignment Scores:
Pred. No.:                7.87e-176      Length:          465
Score:                    1880.00        Matches:         358
Percent Similarity:       84.15%         Conservative:    35
Best Local Similarity:    76.66%         Mismatches:      72
Query Match:              75.62%         Indels:          2
DB:                       4              Gaps:            2

US-09-488-265B-30 (1-1404) x US-09-044-718-80 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60

Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120

Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180

Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240

Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300

Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360

Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420

Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480

Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540

Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600

Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 196

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660

Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720

Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780

Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840

Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900

Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
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Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||    |||||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   ||||||||||||||||||||||||||||||||||:||   ||||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||||||||||||||||||||||||||||||||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||||||||||||   :::|||   ||||||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
              |||||||||   |||||||||||.|   | |   ||||||||||::::::|||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1320
              |||||||||   |||:::||||:|||||||||||||||||||||||||   ||||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||   :::||||||||||:::|||||||||||||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGAAGAATGTTTCGCT 1401
              ||||||   |||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 12
US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-79

Alignment Scores:
Pred. No.:              9.86e-176       Length:         465
Score:                  1879.00         Matches:        358
Percent Similarity:     84.15%          Conservative:   35
Best Local Similarity:  76.66%          Mismatches:     72
Query Match:            75.58%          Indels:         2
DB:                     4               Gaps:           2

US-09-488-265B-30 (1-1404) x US-09-044-718-79 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||               |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA 180
              |||       ||||||||||||||   ||||||||||||||||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ::::::|||       :::||||||   ||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||   ||||||   |||      |||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   |:||||||:   ||||||||||||:::|||:|||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 420
              |||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||||||||||||||||   :::|||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||   ||||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 600
              ||||||||||||||||||||||      :::::|||:::|||   |||:::||||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 660
              ||||||         :::|||||||||||||||||||||:::||||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
              |||:::|||||||||:::|||   |||||||||||||||:::|||||:|||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 780
              ||||||   |||   ||||||||||||||   |||||||||||||||||||||:::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 840
              ||||||||||||   |||||||||||||||||||||||||||||:::|||||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 900
              ||||||   |:|||||||||||:::||||||   :::|||:::|||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||    |||||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   ||||||||||||||||||||||||||||||||||:::|||   ||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1140
              |||||||||:::|||||||||||||||||||||||||||||||||||||||||:::
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378
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Db        249 ArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeuMet 268

Qy        784 GACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTC 843
              |||||||||   |||||||||||||||||||||||||||||||||||:::::::|||||||||||
Db        269 AspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerProPhe 288

Qy        844 TGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGTAAG 903
              |||   |||||||||||||:::|||||   :::|||:::|||||||||||||||||||||
Db        289 CysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLys 308

Qy        904 TACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCTAAC 963
              |||||||||||||||||||||||||||||||||||||||||||||||:::|||||   |||
Db        309 TyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsn 328

Qy        964 GAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACT 1023
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        329 GluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSerThr 348

Qy       1024 TTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCAC 1083
              |||   |||||||||||||||||||||||||||||||||||:::|||   |||||||||||
Db        349 LeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSerHis 368

Qy       1084 GACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTG 1143
              ||||||:::|||:::|||||||||||||||||||||||||||||||||||:::|||| ||
Db        369 AspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeu 388

Qy       1144 TCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTT 1203
              |||   |||||||||||||||   :::|||   |||||||||||||||||||||||   |||
Db        389 SerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValVal 408

Qy       1204 CCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCATTG 1263
              ||||||   |||||||||||   |||   ||||||||||||||||||||||||||||||
Db        409 ProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluProLeu 428

Qy       1264 GTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAGTTG 1323
              ||||||   |||:::|||||||||||||||||||||||||||||   ||||||||||||
Db        429 ValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLysLeu 448

Qy       1324 GGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAAC 1383
              ||||||||||||   :::|||||||||:::|||||||||:::|||||||||||||||||||
Db        449 GlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsn 468

Qy       1384 TGGGCTGAATGTTTCGCT 1401
              |||   |||||||||:::
Db        469 TrpGlyGluCysPheSer 474

RESULT 9
US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
;  APPLICANT: KONDO, HIDEMASA
;  APPLICANT:  ANAZAWA, HIDEHARU
;  APPLICANT:  KANEKO, SYUNICHI
;  APPLICANT:  NAGASHIMA, TADASHI
;  APPLICANT:  TANGE, TATSUYA
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 081356/0166
;  CURRENT APPLICATION NUMBER: US/09/929,060
;  CURRENT FILING DATE:  2001-08-05
;  PRIOR APPLICATION NUMBER: 09/543,744
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: 09/155,855
;  PRIOR FILING DATE: 1998-10-05
;  PRIOR APPLICATION NUMBER: JP 084314/1996
;  PRIOR FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-929-060-3

Alignment Scores:
Pred. No.:              3.59e-151     Length:          467
Score:                  1860.00       Matches:         346
Percent Similarity:     84.37%        Conservative:    48
Best Local Similarity:  74.09%        Mismatches:      73
Query Match:            75.00%        Indels:          0
DB:                     9             Gaps:            0

US-09-488-265B-28 (1-1404) x US-09-929-060-3 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||||||||   |||||||||   :::   |||   |||   |||||||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||:::             |||      :::|||||||||||||||   ||||||||||:
Db         21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||   |||||||||||:||||   ||||:::|||:::|||||||||||::::::
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnLys 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||||||||||||||||||||||||   |||   |||||||||   |||||||||||
Db         61 SerAlaIleSerProAspValProAlaGlyCysHisValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              |||||||||||||||||||||||||   |||   |||   ||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||:::|||||||||   |||:::|||||||||||||||||||||||||||||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||:::|||||||||||||||||||||||||||||||||||||   ::::::||||||||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              :::|||||||||:::||||||:::::|||   |||   ||||||||||||||||||:::
Db        141 ValLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||   |||||||||||||||      ||||||||||||||||||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||   ||||||   :::||||||   |||:::||||||   |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
              |||   |||      ||||||||||||||   ||||||||||   ||||||||
Db        201 SerGluAlaSerThrSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||||||||   ||||||:::|||||||||||||||||||||   |||   |||:::||||||
Db        221 SerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              |||||||||   ||||||   ||||||:::|||||||||   :::|||   ||||||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValSerLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||   ||||||||||::::::   ::::::      |||:::|||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   ||||||||||||:::|||||||||   ||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisGluGluTrpIleAsnTyrAspTyrLeuGlnSerLeuAsn 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||:::|||||||||||||||||||||||||||   ||||||||||||:::|||
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Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||||||||||   |||   ||||||:::||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              |||||||||   :::||||||||||   |||||||||||||||||||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||:::|||:::   |||:::|||   :::|||||||||:::|||:::::::||||||
Db        381 LeuSerSerThrThrAlaGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              ||||||||||||:::|||   ||||||||||||||||||||||||||:::|||:::|||||||
Db        401 ValProPheAlaSerArgMetTyrValGluMetMetGlnCysGlnSerGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   ||||||   ||||||:::|||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValLysGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              :::|||   |||:|||||||||
Db        461 AspTrpGlyGluCysPheAla 467

RESULT 10
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-80

Alignment Scores:
Pred. No.:              4.37e-151       Length:         465
Score:                  1859.00         Matches:        354
Percent Similarity:     83.51%          Conservative:   36
Best Local Similarity:  75.80%          Mismatches:     75
Query Match:            74.96%          Indels:         2
DB:                     15              Gaps:           2

US-09-488-265B-28 (1-1404) x US-10-062-848-80 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||               |||||||||   |||   |||

Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||           ||    |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||      ||||||||||||||   ||||||||:::||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ::::::::|||      :::|||   ||||||||:::|||   ||||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||||   ||||||   |||      |||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   |||||||||   ||||||||||||:::|||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||||||||||||||||||||||||||||||||||||||||   |||:::||||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||:::|||||||||||||||||||||   :::||||||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||   ||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||||||||||||||:::      :::::::|||:::|||   |||:::|||||||||
Db        180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
              ||||||         :::|||||||||||||||||||||   ||||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||:::|||||||||:::|||   ||||||||||||||||||||||||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              :|||||   |||      |||||||||||||||||||||||||||||||||||   |||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||   ||||||||||||||||||||||||||||||:::::|||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   ||||||||||||:::|||||   :::|||:::|||||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   ||||||||||||||||||||||||||||||||||||:::|||   ||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              |||||||||:::|||:::||||||||||||||||||||||||||||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
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Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465
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RESULT 11
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Alignment Scores:

Pred. No.:	5.33e-151	Length:	465
Score:	1858.00	Matches:	354
Percent Similarity:	83.51%	Conservative:	36
Best Local Similarity:	75.80%	Mismatches:	75
Query Match:	74.92%	Indels:	2
DB:	15	Gaps:	2

US-09-488-265B-28 (1-1404) x US-10-062-848-79 (1-465)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
Db        180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
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Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 12
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-3

Alignment Scores:
Pred. No.:              5.74e-151       Length:         439
Score:                  1857.50         Matches:        347
Percent Similarity:     87.05%          Conservative:   36
Best Local Similarity:  78.86%          Mismatches:     56
Query Match:            74.90%          Indels:         1
DB:                     15              Gaps:           1

US-09-488-265B-28 (1-1404) x US-10-062-848-3 (1-439)

Qy         82 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 141
Db          1 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 20

Qy        142 TGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGTT 201
Db         21 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 40

Qy        202 CCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 261
Db         41 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 60

Qy        262 ACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 321
Db         61 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 80

Qy        322 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 381
Db         81 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 100

Qy        382 TTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 441
Db        101 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 120

Qy        442 AAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTATT 501
Db        121 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 140

Qy        502 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTTCT 561
Db        141 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 160

Qy        562 CAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATTCCAGAAGGATCCGGTTACAAC 621
Db        161 ---ThrAsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 179

Qy        622 AACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGACTCTGAATTAGGTGACGACGTT 681
Db        180 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 199

Qy        682 GAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTG 741
Db        200 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 219

Qy        742 CCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGAC 801
Db        220 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 239

Qy        802 ACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTTTGTTCACTCAC 861
Db        240 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 259

Qy        862 GACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGTAAGTACTACGGTTACGGTGCT 921
Db        260 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 279

Qy        922 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCTAACGAATTGATTGCTAGATTG 981
Db        280 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 299

Qy        982 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1041
Db        300 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 319

Qy       1042 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATCT 1101
Db        320 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 339

Qy       1102 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTACTTCTGTTGAA 1161
Db        340 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 359

Qy       1162 TCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1221
Db        360 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 379

Qy       1222 TACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1281
Db        380 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 399

Qy       1282 GACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1341
Db        400 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 419

Qy       1342 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGCT 1401
Db        420 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 439

RESULT 13
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
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;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Alignment Scores:
Pred. No.:                5.79e-151      Length:          449
Score:                    1857.50        Matches:         347
Percent Similarity:       87.05%         Conservative:    36
Best Local Similarity:    78.86%         Mismatches:      56
Query Match:              74.90%         Indels:          1
DB:                       15             Gaps:            1

US-09-488-265B-28 (1-1404) x US-10-062-848-12 (1-449)

Qy         82 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 141
              |||   |||||||||||||||||   ||||||||||   |||      ||||||||:|
Db         11 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 30

Qy        142 TGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGACGTT 201
              ||||||   ||||||||||:::|||||||   |||||   :::::::|||      :::
Db         31 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 50

Qy        202 CCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 261
              |||   |||||||||:::|||   ||||||||||||||||||||||||||||:||||
Db         51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70

Qy        262 ACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 321
              |||||||||   ||||||   |||      |||:::   ||||||||||   ||||:|||
Db         71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90

Qy        322 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 381
                 ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||
Db         91 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110

Qy        382 TTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 441
              ||||||||||||||||   |||:::|||||||||||||:|||||||||||:::|||||
Db        111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130

Qy        442 AAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTTATT 501
              |||||||||||||||   :::|||||||||||||||||||||||||||||||||||||
Db        131 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 150

Qy        502 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTTCT 561
              ||||||   ||||||||||||||||||||||   ||||||||||:||||||||:::
Db        151 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 170

Qy        562 CAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATTCCAGAAGGATCCGGTTACAAC 621
                  ::::::|||:::|||   |||:::|||||||||||||||      :::|||
Db        171 ---ThrAsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189

Qy        622 AACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGACTCTGAATTAGGTGACGACGTT 681
              ||||||||||||||||   ||||||   ||||||   |||:::|||||||:::|||
Db        190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209

Qy        682 GAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTG 741
                 |||||||||||||||||||||||||   ||||||||||||   |||      |||
Db        210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 229

Qy        742 CCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTCGAC 801
              ||||||||||||||||||||||||||||||;|||   ||||||||||||;|||   ||||||
Db        230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249

Qy        802 ACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTTTGTTCACTCAC 861
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                 ||||||||||||||||||||||||:::::|||||||||||||||   ||||||||||||
Db        250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269

Qy        862 GACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGTAAGTACTACGGTTACGGTGCT 921
              :::|||||   :::|||:::|||||||||||||||||||||||||||||||||||||||
Db        270 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 289

Qy        922 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCTAACGAATTGATTGCTAGATTG 981
              ||||||||||||||||||||||||||:::||||||   ||||||||||||||||||||
Db        290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309

Qy        982 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1041
              |||   ||||||||||||||||||||||||||||   ||||||   ||||||||||||
Db        310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329

Qy       1042 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATATCT 1101
              ||||||||||||||||||||||:::|||   ||||||||||||||||:::||||||||||
Db        330 ThrProProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 349

Qy       1102 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTACTTCTGTTGAA 1161
              ||||||||||||||||||||||||||||||:::|||||||||   ||||||||||||
Db        350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 369

Qy       1162 TCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1221
              |||   :::|||   ||||||||||||||||||||   |||||||||   ||||||||||
Db        370 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 389

Qy       1222 TACGTTGAAATGATGCAAATGTCAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1281
              |||   |||   ||||||||||:::::|||||||||||||||||||||   |||:::|||
Db        390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409

Qy       1282 GACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1341
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||   :::
Db        410 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 429

Qy       1342 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTCGCT 1401
              |||||||||:::|||||||||:::|||||||||||||||||||||   |||||||||:::
Db        430 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 449

RESULT 14
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Alignment Scores:
Pred. No.:                9.64e-151      Length:          465
Score:                    1855.00        Matches:         353
Percent Similarity:       83.51%         Conservative:    37
Best Local Similarity:    75.59%         Mismatches:      75
Query Match:              74.80%         Indels:          2
DB:                       15             Gaps:            2
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US-09-488-265B-28 (1-1404) x US-10-062-848-81 (1-465)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||           |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||            |||   |||   |||,|||||||||||||||   ||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
                 |||      |||||||||||||||   |||||||||:::|||||||||   |||| |
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              :::::::|||      :::|||   ||||||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              |||||||||||||||||||||||||||||   ||||||   |||      |||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              |||||||||   |||||||||   |||||||||||:::|||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||||||||||||||||||||||||||   |||||||||   |||:::|||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrAlaPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||||||||||||||||   :::|||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||||||||||||||:::      :::::::|||:::|||   |||:::||||||||
Db        180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
              ||||||         :::|||'||||||||||||||||||   ||||||   |||| |
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||:::||||||||:::|||   ||||||||||||||||||||||||||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              ||||||   :::      ||||,||||||||||||||||||||||||||||   |||
Db        239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||   |||||||.|||||||||||||||||||||:::::::|'|||'|||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   ||||||||||||:::||||||   :::|||:::|||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              |||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||   |||||||||||||||||||||||||||||||||:::|||   |||||||||

Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              ||||||||||:::|||:::|||||||||||||||||||||||||||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||   ||||||||||||||||   :::|||   ||||||||||||||||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              |||||||||   ||||||||||||   |||   |||||||||:::::::||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              |||||||||   |||:::|||||||||||||||||||||||||||||||   |||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||   :::||||||||||:::||||||||:::||||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              ||||||   ||||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 15
US-10-229-358-12
; Sequence 12, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 462
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-229-358-12

Alignment Scores:
Pred. No.:              2.12e-150       Length:         462
Score:                  1851.00         Matches:        349
Percent Similarity:     84.42%          Conservative:   41
Best Local Similarity:  75.54%          Mismatches:     72
Query Match:            74.64%          Indels:         0
DB:                     15              Gaps:           0

US-09-488-265B-28 (1-1404) x US-10-229-358-12 (1-462)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              |||||||||      |||||||||   :::      |||   |||   |||||||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||:::            |||      ||||||||||||||||   ||||||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||   ||||||||||||||   |||:::|||:::||||||||||||:::|||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||   |||||||||:::||||||      ||||||||||||||   ||||||||||||
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Db        61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy       241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
Db        81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy       301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db       101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy       361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
Db       121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy       421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db       141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy       481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db       161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy       541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
Db       181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy       601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db       201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy       661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db       221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheAlaProSerIleArg 240

Qy       721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db       241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy       781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db       261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy       841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db       281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy       901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db       301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy       961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db       321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy      1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db       341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy      1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db       361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy      1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db       381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy      1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db       401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy      1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db       421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy      1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db       441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy      1381 AACTGG 1386
Db       461 AspTrp 462
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Search completed: October 3, 2003, 09:05:52
Job time : 94.6311 secs

GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 07:48:21 ; Search time 21.0567 Seconds
(without alignments)
5642.336 Million cell updates/sec

Title: US-09-488-265B-28
Perfect score: 2480
Sequence: 1 atgggcgtgttcgtcgtgct.....gggctgaatgtttcgcttaa 1404

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=oct3.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265_@CGN_1_1_99_@runat_03102003_074813_12239 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2408	97.1	467	4	US-09-273-871A-9	Sequence 9, Appli
2	2282	92.0	441	3	US-09-121-425-1	Sequence 1, Appli
3	2282	92.0	441	4	US-09-634-493A-1	Sequence 1, Appli
4	2270	91.5	467	3	US-09-121-425-2	Sequence 2, Appli
5	2270	91.5	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1879	75.8	467	1	US-07-923-724-8	Sequence 8, Appli
7	1879	75.8	467	2	US-08-609-426A-8	Sequence 8, Appli
8	1879	75.8	467	2	US-08-374-652C-2	Sequence 2, Appli
9	1875	75.6	467	1	US-08-151-574-32	Sequence 32, Appl
10	1875	75.6	467	1	US-08-146-424-20	Sequence 20, Appl
11	1875	75.6	467	1	US-08-693-709-2	Sequence 2, Appli
12	1875	75.6	467	2	US-08-419-448-32	Sequence 32, Appl
13	1875	75.6	467	2	US-08-819-825-3	Sequence 3, Appli
14	1875	75.6	467	3	US-09-163-642-3	Sequence 3, Appli
15	1875	75.6	467	4	US-09-233-510-32	Sequence 32, Appl
16	1875	75.6	467	4	US-09-636-499-5	Sequence 5, Appli
17	1867	75.3	465	3	US-08-868-435-33	Sequence 33, Appl
18	1867	75.3	465	4	US-08-744-231-33	Sequence 33, Appl
19	1867	75.3	465	4	US-09-044-718-78	Sequence 78, Appl
20	1867	75.3	465	4	US-09-636-499-6	Sequence 6, Appli
21	1867	75.3	465	4	US-09-273-871A-8	Sequence 8, Appli
22	1863	75.1	467	4	US-09-273-871A-11	Sequence 11, Appl
23	1860	75.0	467	3	US-09-155-855-3	Sequence 3, Appli
24	1860	75.0	467	4	US-09-543-744-3	Sequence 3, Appli
25	1860	75.0	467	4	US-09-929-060-3	Sequence 3, Appli
26	1859	75.0	465	4	US-09-044-718-80	Sequence 80, Appl
27	1858	74.9	465	4	US-09-044-718-79	Sequence 79, Appl
28	1857.5	74.9	439	4	US-09-044-718-3	Sequence 3, Appli
29	1857.5	74.9	449	4	US-09-044-718-12	Sequence 12, Appl
30	1855	74.8	465	4	US-09-044-718-81	Sequence 81, Appl
31	1851	74.6	462	4	US-09-636-499-12	Sequence 12, Appl
32	1845	74.4	469	4	US-09-044-718-82	Sequence 82, Appl
33	1839	74.2	466	3	US-08-868-435-35	Sequence 35, Appl
34	1839	74.2	466	4	US-08-744-231-35	Sequence 35, Appl
35	1835.5	74.0	463	3	US-08-868-435-29	Sequence 29, Appl
36	1835.5	74.0	463	4	US-08-744-231-29	Sequence 29, Appl
37	1835.5	74.0	463	4	US-09-273-871A-10	Sequence 10, Appl
38	1833	73.9	444	4	US-09-044-718-1	Sequence 1, Appli
39	1820.5	73.4	447	4	US-09-044-718-6	Sequence 6, Appli
40	1818	73.3	443	3	US-09-155-855-1	Sequence 1, Appli
41	1818	73.3	443	4	US-09-543-744-1	Sequence 1, Appli
42	1818	73.3	443	4	US-09-929-060-1	Sequence 1, Appli
43	1813	73.1	443	3	US-09-155-855-2	Sequence 2, Appli
44	1813	73.1	443	4	US-09-543-744-2	Sequence 2, Appli
45	1813	73.1	443	4	US-09-929-060-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Alignment Scores:

Pred. No.:	2.7e-236	Length:	467
Score:	2408.00	Matches:	457
Percent Similarity:	98.50%	Conservative:	3

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Best Local Similarity:  97.86%        Mismatches:    7
Query Match:            97.10%        Indels:        0
DB:                     4             Gaps:          0

US-09-488-265B-28 (1-1404) x US-09-273-871A-9 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
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Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              ||||||||||||||||||||||||||  ||||||||||||||||||||  ||||||||||
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              |||||||||||||||||||||
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

Alignment Scores:
Pred. No.:              1.75e-223     Length:        441
Score:                  2282.00       Matches:       431
Percent Similarity:     98.41%        Conservative:  3
Best Local Similarity:  97.73%        Mismatches:    7
Query Match:            92.02%        Indels:        0
DB:                     3             Gaps:          0

US-09-488-265B-28 (1-1404) x US-09-121-425-1 (1-441)

Qy         79 AATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCAC 138
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20

Qy        139 TTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGAC 198
              ||||||||||  ||||||||||||||||||||  ||||||||||||||||||||||||||
Db         21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40

Qy        199 GTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATAC 258
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60
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Qy       259 CCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCT 318
Db        61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80

Qy       319 ACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
Db        81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

Qy       379 GACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGA 438
Db       101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120

Qy       439 TACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTT 498
Db       121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140

Qy       499 ATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGT 558
Db       141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160

Qy       559 TCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATTCCAGAAGGATCCGGTTAC 618
Db       161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180

Qy       619 AACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGACTCTGAATTAGGTGACGAC 678
Db       181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

Qy       679 GTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGAC 738
Db       201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220

Qy       739 TTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTC 798
Db       221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240

Qy       799 GACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTTTGTTCACT 858
Db       241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260

Qy       859 CACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGTAAGTACTACGGTTACGGT 918
Db       261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280

Qy       919 GCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCTAACGAATTGATTGCTAGA 978
Db       281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

Qy       979 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCA 1038
Db       301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320

Qy      1039 GCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATA 1098
Db       321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340

Qy      1099 TCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTACTTCTGTT 1158
Db       341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360

Qy      1159 GAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGA 1218
Db       361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380

Qy      1219 GCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
Db       381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

Qy      1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGA 1338
Db       401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420

Qy      1339 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTC 1398
Db       421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440

Qy      1399 GCT 1401
Db       441 Ala 441
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RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-1

Alignment Scores:

Pred. No.:	1.75e-223	Length:	441
Score:	2282.00	Matches:	431
Percent Similarity:	98.41%	Conservative:	3
Best Local Similarity:	97.73%	Mismatches:	7
Query Match:	92.02%	Indels:	0
DB:	4	Gaps:	0

US-09-488-265B-28 (1-1404) x US-09-634-493A-1 (1-441)

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Qy        79 AATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCAC 138
Db         1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis 20

Qy       139 TTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAATCTGCTATTTCTCCAGAC 198
Db        21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40

Qy       199 GTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATAC 258
Db        41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60

Qy       259 CCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCT 318
Db        61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80

Qy       319 ACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 378
Db        81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

Qy       379 GACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGA 438
Db       101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120

Qy       439 TACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGGTTCTGACAGAGTT 498
Db       121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140

Qy       499 ATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGT 558
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Db        141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160

Qy        559 TCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATTCCAGAAGGATCCGGTTAC 618
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180

Qy        619 AACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGACTCTGAATTAGGTGACGAC 678
              ||'|||:|||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

Qy        679 GTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGAC 738
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||| ||
Db        201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220

Qy        739 TTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTGATGGACATGTGTCCATTC 798
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240

Qy        799 GACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCATTCTGTGCTTTGTTCACT 858
              :::|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260

Qy        859 CACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGTAAGTACTACGGTTACGGT 918
              ||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Db        261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280

Qy        919 GCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCTAACGAATTGATTGCTAGA 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

Qy        979 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCA 1038
              ||:|||   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320

Qy       1039 GCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGATA 1098
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Db        321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340

Qy       1099 TCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCATTGTCTACTACTTCTGTT 1158
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360

Qy       1159 GAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGA 1218
              ||||||||||||||||||||||||||||||:|||||||||||||||||||   ||||||
Db        361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380

Qy       1219 GCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

Qy       1279 AACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAGTTGGGTAGATGTAAGAGA 1338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420

Qy       1339 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGCTGAATGTTTC 1398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440

Qy       1399 GCT 1401
              |||
Db        441 Ala 441

RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2

Alignment Scores:
Pred. No.:                3.03e-222       Length:          467
Score:                    2270.00         Matches:         437
Percent Similarity:       90.35%          Conservative:    3
Best Local Similarity:    89.73%          Mismatches:      7
Query Match:              91.53%          Indels:          40
DB:                       3               Gaps:            2

US-09-488-265B-28 (1-1404) x US-09-121-425-2 (1-467)

Qy           1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy          61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy         121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
               |||||||||||||||||||||||||||   ||||||||||||||||||   ||||||
Db          41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy         181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy         241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
               |||||||||||||||||||||||||||||   ||||||||||||||||
Db          81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla--------- 97

Qy         301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
                                                                 ||||||||
Db          98 ----------------------------------------------------ThrTyrAsn 100

Qy         361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120

Qy         421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140

Qy         481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160

Qy         541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAAC--------- 591
               ||||||||||||||||||||||||||||||||||||||||||||||||:::
Db         161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

Qy         592 ----------------------------------------------------GTGATCATT 600
                                                                   |||||||||
Db         181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200

Qy         601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy         661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
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Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-2

Alignment Scores:
Pred. No.:              3.03e-222       Length:         467
Score:                  2270.00         Matches:        437
Percent Similarity:     90.35%          Conservative:   3
Best Local Similarity:  89.73%          Mismatches:     7
Query Match:            91.53%          Indels:         40
DB:                     4               Gaps:           2

US-09-488-265B-28 (1-1404) x US-09-634-493A-2 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla--------- 97

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db         98 ----------------------------------------------------ThrTyrAsn 100

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
Db        101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAAC--------- 591
Db        161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

Qy        592 ----------------------------------------------------GTGATCATT 600
Db        181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
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Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||    ||||||||||||||||||||||| ||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              |||||||||    ||||||||||||||||||||||||||||||||||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              |||||||||||||||||||||
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 6
US-07-923-724-8
; Sequence 8, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
;   APPLICANT:  Nevalainen, Helena K.M.
;   APPLICANT:  Paloheimo, Marja T.
;   APPLICANT:  Miettinen-Oinonen, Arja S.K.
;   APPLICANT:  Torkkeli, Tuula K.
;   APPLICANT:  Cantrell, Michael
;   APPLICANT:  Piddington, Christopher S.
;   APPLICANT:  Rambosek, John A.
;   APPLICANT:  Turunen, Marja K.
;   APPLICANT:  Fagerstr m, Richard B.
;   TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;   TITLE OF INVENTION:  in Trichoderma
;   NUMBER OF SEQUENCES:  66
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;     STREET:  1100 New York Avenue, Suite 600
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  U.S.A.
;     ZIP:  20005
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/07/923,724
;     FILING DATE:  31-JUL-1992
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/496,155
;     FILING DATE:  19-MAR-1990
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/044,077
;     FILING DATE:  29-APR-1987
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  UK 8610600
;     FILING DATE:  30-APR-1986
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Cimbala, Michele A.
;     REGISTRATION NUMBER:  33,851
;     REFERENCE/DOCKET NUMBER:  1050.0240004
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (202) 371-2600
;     TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  467 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-07-923-724-8

Alignment Scores:
Pred. No.:                1.93e-182       Length:          467
Score:                    1879.00         Matches:         353
Percent Similarity:       84.37%          Conservative:    41
Best Local Similarity:    75.59%          Mismatches:      73
Query Match:              75.77%          Indels:          0
DB:                       1               Gaps:            0

US-09-488-265B-28 (1-1404) x US-07-923-724-8 (1-467)

Qy           1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
               |||||||||      |||||||||  :::      |||  |||  |||||||||
Db           1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValThrSerGlyLeu 20

Qy          61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
               ||||::      |||      :::||||||||||||||||  ||||||||||||
Db          21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40

Qy         121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
               |||  |||  |||||||||||||||  |||::::|||:::|||||||||||:::|||
Db          41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy         181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
               |||||||||||||||||||||      ||||||||||||||  ||||||||||||
Db          61 SerAlaIleSerProAspValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy         241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
               ||||||||||||||||||||||:|  |||      |||  ||||:|||||||||||||
Db          81 ArgHisGlyAlaArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy         301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
                 |:||||:::|||  |||  |||  ||||||||||||||||||||||||||||||||
Db         101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy         361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
               |||:|||||||||||||||||||||||||||||||||||  :::::|||||||||||||
Db         121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy         421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
               |||||||||||:::|||||:::::|||  ||,  |||:::|||||||||||||:::
Db         141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleIleProPheIleArgSer 160

Qy         481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
               |||||||  ||||||||||:||||  ||||||||||||||:|||||||||||||||||
Db         161 SerGlySerSerArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnSerThr 180

Qy         541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
               ||||||  ||||||  :::|||||||  |||:::||||||  |||:::|||:::|||
Db         181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy         601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
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Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheAlaProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1021
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProIleAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
Db        461 AspTrpAlaGluCysSerAla 467

RESULT 7
US-08-609-426A-8
; Sequence 8, Application US/08609426A
; Patent No. 5830733
;  GENERAL INFORMATION:
;    APPLICANT:  Nevalainen, Helena K.M.
;    APPLICANT:  Paloheimo, Marja T.
;    APPLICANT:  Miettinen-Oinonen, Arja S.K.
;    APPLICANT:  Torkkeli, Tuula K.
;    APPLICANT:  Cantrell, Michael
;    APPLICANT:  Piddington, Christopher S.
;    APPLICANT:  Rambosek, John A.
;    APPLICANT:  Turunen, Marja K.
;    APPLICANT:  Fagerstr m, Richard B.
;    APPLICANT:  Houston, Christine S.
;    TITLE OF INVENTION:  Production of Phytase Degrading Enzymes
;    TITLE OF INVENTION:  in Trichoderma
;    NUMBER OF SEQUENCES:  69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox
;      STREET:  1100 New York Avenue, Suite 600
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/609,426A
;      FILING DATE:  01-MAR-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/923,724
;      FILING DATE:  31-JUL-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/496,155
;      FILING DATE:  19-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/044,077
;      FILING DATE:  29-APR-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  UK 8610600
;      FILING DATE:  30-APR-1986
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Reed, Grant E.
;      REGISTRATION NUMBER:  P-41,264
;      REFERENCE/DOCKET NUMBER:  1050.008000I
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 371-2600
;      TELEFAX:  (202) 371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-609-426A-8

Alignment Scores:
Pred. No.:                1.93e-182       Length:          467
Score:                    1879.00         Matches:         353
Percent Similarity:       84.37%          Conservative:    41
Best Local Similarity:    75.59%          Mismatches:      73
Query Match:              75.77%          Indels:          0
DB:                       2               Gaps:            0

US-09-488-265B-28 (1-1404) x US-08-609-426A-8 (1-467)

Qy           1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db           1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValThrSerGlyLeu 20

Qy          61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db          21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40

Qy         121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
Db          41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy         181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db          61 SerAlaIleSerProAspValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy         241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
Db          81 ArgHisGlyAlaArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
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Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleIleProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        161 SerGlySerSerArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheAlaProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProIleAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
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                 Db        461 AspTrpAlaGluCysSerAla 467

RESULT 8
US-08-374-652C-2
; Sequence 2, Application US/08374652C
; Patent No. 5834286
; GENERAL INFORMATION:
;   APPLICANT:  NEVALAINEN, HELENA K.M.
;   APPLICANT:  PALOHEIMO, MARJA T.
;   APPLICANT:  PAGERSTROM, RICHARD B.
;   APPLICANT:  MIETTINEN-OINONEN, ARJA S.
;   APPLICANT:  TURUNEN, MARJA K.
;   APPLICANT:  RAMBOSEK, JOHN A.
;   APPLICANT:  PIDDINGTON, CHRISTOPHER S.
;   APPLICANT:  HOUSTON, CHRISTINE S.
;   APPLICANT:  CANTRELL, MICHAEL A.
;   TITLE OF INVENTION:  RECOMBINANT CELLS, DNA CONSTRUCTS,
;   TITLE OF INVENTION:  VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
;   TITLE OF INVENTION:  ENZYMES IN DESIRED RATIOS
;   NUMBER OF SEQUENCES:  94
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;     STREET:  1100 NEW YORK AVENUE, SUITE 600
;     CITY:  WASHINGTON
;     STATE:  DC
;     COUNTRY:  USA
;     ZIP:  20005
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/374,652C
;     FILING DATE:  24-MAY-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US93/07058
;     FILING DATE:  27-JUL-1993
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 07/925,401
;     FILING DATE:  31-JUL-1992
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  REED, GRANT E.
;     REGISTRATION NUMBER:  41,264
;     REFERENCE/DOCKET NUMBER:  1050.071001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  202-371-2600
;     TELEFAX:  202-371-2540
; INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  467 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  not relevant
;   MOLECULE TYPE:  protein
US-08-374-652C-2

Alignment Scores:
Pred. No.:                1.93e-182       Length:          467
Score:                    1879.00         Matches:         353
Percent Similarity:       84.37%          Conservative:    41
Best Local Similarity:    75.59%          Mismatches:      73
Query Match:              75.77%          Indels:          0
DB:                       2               Gaps:            0

US-09-488-265B-28 (1-1404) x US-08-374-652C-2 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
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Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         61 SerAlaIleSerProAspValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
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Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
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Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
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Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        161 SerGlySerSerArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIleIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheAlaProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleHisTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
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Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProIleAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
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Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
Db        461 AspTrpAlaGluCysSerAla 467
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RESULT 9
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-151-574-32

Alignment Scores:

Pred. No.:	4.93e-182	Length:	467
Score:	1875.00	Matches:	353
Percent Similarity:	84.37%	Conservative:	41

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Best Local Similarity:  75.59%        Mismatches:    73
Query Match:            75.60%        Indels:        0
DB:                     1             Gaps:          0

US-09-488-265B-28 (1-1404) x GS-08-151-574-32 (1-467)

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Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||:::           |||      ||||||||||||||||||   ||||||||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||   ||||||||||||||:   |||:::|||:::||||||||||||:::|||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||   ||||||||:::|||||       ||||||||||||||||   |:|||  ||||||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              |||||||||||||||:|||||||||   |||       |||   |||:|||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||:::|||||||||   |||   ||||||||||||||||||||||||||||||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||:::||||||||||||||||||||||||||||||||||   ::::::|||||||||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||||:::||||||:::::|||   |||   |||||||||||||||||:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||   ||||||||||||||||   :::|||||||||||||||||||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
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Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

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              |||   |||      ||||||||||||||||   ||||||||||||   ||||||||||
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
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Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              |||||||||   ||||||   ||||||||||||||||||   :::|||   ||||||||||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||:||||||:|   |||||||||:::::::   ::::::      ||||:::|||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   ||||||||||||||||||||||||||   ||||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
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Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||||||||   |||   ||||||:::|||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||:::|||||||||||||||||||||||:::|||||||||||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              |||||||||   :::||||||||||   ||||||||||||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              |||||||||||:::||||||:::|||   :::|||||||:|:::|||||||||||||||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              |||||||,||||:::|||   ||||||||||||:|||||||||||||||||:::|||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
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Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   ||||||   ||||||   ||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              :::|||||||||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 10
US-08-146-424-20
; Sequence 20, Application US/08146424
; Patent No. 5593963
;  GENERAL INFORMATION:
;    APPLICANT:  VAN OOIJEN, ALBERT J. J.
;    APPLICANT:  RIETVELD, KRIJN
;    APPLICANT:  HOEKEMA, ANDREAS
;    APPLICANT:  PEN, JAN
;    APPLICANT:  SIJMONS, PETER C.
;    APPLICANT:  VERWOERD, TEUNIS C.
;    TITLE OF INVENTION:  THE EXPRESSION OF PHYTASE IN PLANTS
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/146,424
;      FILING DATE:  02-NOV-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KENNEDY, BILL
;      REGISTRATION NUMBER:  33,407
;      REFERENCE/DOCKET NUMBER:  44615-20011.24
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-146-424-20
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Alignment Scores:

Pred. No.:	4.93e-182	Length:	467
Score:	1875.00	Matches:	353
Percent Similarity:	84.37%	Conservative:	41
Best Local Similarity:	75.59%	Mismatches:	73
Query Match:	75.60%	Indels:	0
DB:	1	Gaps:	0

US-09-488-265B-28 (1-1404) x US-08-146-424-20 (1-467)

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Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
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Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||:::          |||       ||||||||||||||||!    ||||||||||.
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||   ||||||||||||||   |||:::|||:::|||||:|||:::::||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||   |||||||:|:::|||||      ||||||||||||||   ||||||||||.|
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              ||||||||||||||||:|||||:   |||      |||   ||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
                 |||||||:::|||||||||   |||   |||||||||:|||||||:|||||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||:::|||||||||||||||||||||||||||||||||   ::::::|||||||||  ||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||:::|||||:::::::|||   |||   ||||||||||| |||:|:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||   ||||||||:|||||   :::|||||||||||||||||:|||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||   |||||   :::|||||||   |||:::|||||   ||||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
                 |||   |||       |||||||||||||||   ||||||||||||   |||||||||
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||||||||   |||   |||||||||||||||||||||   |||   ||||:|||||
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
                 |||||||||   ||||||   |||||||||||||||||||   :::|||   ||||||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||   ||||||||||::::::   ::::::      ||||:|||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   |||||||||||||||||||||||   ||||||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||:::|||||||||||||||||||||||||   ||||||||||||:::|||
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Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||:|||||||||||||||||||||||||||||||   |||   ||||||:::||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||:::|||||||||||||||||||||||||:::|||||||||||||||||!
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              |||||||||   :::|||||||||   |||||||||||||||||||||||||||||:|
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              |||||||||||:::|||||:::|||   :::|||||||:::|||:::::|||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              |||||||||||:::|||   |||||||||||||||||||||||||||||:::|||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              |||||||||||   ||||||   ||||||   |||:|||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              :::|||||||||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467
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RESULT 11
US-08-693-709-2
; Sequence 2, Application US/08693709
; Patent No. 5770413
; GENERAL INFORMATION:
; APPLICANT: VAN OOIJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,709
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600

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;      TELEFAX:  415-494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FRAGMENT TYPE:  internal
;    FEATURE:
;      NAME/KEY:  Signal Sequence
;      LOCATION:  1...23
;      OTHER INFORMATION:
US-08-693-709-2

Alignment Scores:
Pred. No.:              4.93e-182      Length:          467
Score:                  1875.00        Matches:         353
Percent Similarity:     84.37%         Conservative:    41
Best Local Similarity:  75.59%         Mismatches:      73
Query Match:            75.60%         Indels:          0
DB:                     1              Gaps:            0

US-09-488-265B-28 (1-1404) x US-08-693-709-2 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
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Qy         61 GCCITGGGTCCTCGIGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
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Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
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Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
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Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
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Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
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Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
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Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
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Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||  ||||||||||||||  :::||||||||||||||||:|||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||  ||||||  :::|||||||  |||:::|||||||  |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCCAAGAC 660
              |||  |||      ||||||||||||||  ||||||||||  ||||||||
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||||||||  |||  ||||||||||||||||||||  |:|  |||:::||||||
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              |||||||||  ||||||  ||||||||||||||||||  :::|||  ||||||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||||  ||||||||||::::::  ::::::      |||:::||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||  ||||||||||||||||||||||  ||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              |:||||||||||:::||||||||||:||||||||||  ||||||||:|||:::|||
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||:::|||||||||||||||||||||:::||:|||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTITGTACGCTGACTTCTCT 1080
              ||||||||||||:::|||||||||||||||||||:::||:|||||||||||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
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Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||:::||||||:::|||  :::|||||||||||:::|:::::||||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              ||||||||||:::|||  ||||||||||||||||||||||||||||:::||||||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              ||||||||||||||||||'||||||||||||||||||||||||||||  ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||  ||||||  ||||||  ||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              :::|||||||||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 12
US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
;   APPLICANT:  Robert F.M. Van Gorcom
;   APPLICANT:  Willem Van Hartingsveldt
;   APPLICANT:  Petrus A. Van Paridon
;   APPLICANT:  Annemarie E. Veenstra
;   APPLICANT:  Rudolf G.M. Luttin
;   APPLICANT:  Gerardus Selten
;   TITLE OF INVENTION:  Cloning and Expression of Microbial
;   TITLE OF INVENTION:  Phytase
;   NUMBER OF SEQUENCES:  52
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Morrison & Foerster
;     STREET:  2000 Pennsylvania Ave. N.W., Suite 5500
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  USA
;     ZIP:  20006-1888
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/419,448
;      FILING DATE:  10-APR-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-419-448-32

Alignment Scores:
Pred. No.:              4.93e-182       Length:         467
Score:                  1875.00         Matches:        353
Percent Similarity:     84.37%          Conservative:   41
Best Local Similarity:  75.59%          Mismatches:     73
Query Match:            75.60%          Indels:         0
DB:                     2               Gaps:           0

US-09-488-265B-28 (1-1404) x US-08-419-448-32 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
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Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              |||:::           |||      ||||||||||||||||||   |||||  ||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||  |||||.|||||||||   |||:::|||:::||||||||||''::::||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
              |||   |||||||||:::|||||      ||||||||||||||   ||||||||||||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||   |||      |||   ||||||||||:|||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
              ||||||:::|||||||||   |||   ||||||| ||||||||||||||||||||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||:::|||||||||||||:|||||||||||||||||||   ::::::|||||:|||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              |||||||||.||:::||||||:::::::|||   |||   :||||||||||||||||:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||   ||||||||||||||   :::||||||||||||||||||||||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||   ||||||   :::||||||   |||:::||||||   |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
              |||   |||      ||||||||||||||   ||||||||||||   |||||||||
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||||||||   |||   ||||||||||||||||||||||   |||   |||:::|||||
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATCGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              |||||||||   ||||||   ||||||||||:|||||||   :::|||   ||||||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              |||||||||||   |||||||||::::::   ::::::      |||:::|||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              |||||   |||||||||||||||||||||||||   ||||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||:::|||||||||||||||||||||   ||||||||||||:::|||||
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||||||   |||   ||||||:::||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              |||||||||.||:::|||||||||||||||||||||||:::|||||||||||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              |||||||||   :::|||||||||   ||||:|||||||||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||:::|||||||:::|||   :::|||||||||:::|||:::::|||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              ||||||||||||:::|||   |||||||||:|||||||||||||||||||:::|||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   ||||||   ||||||   ||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              :::|||||||||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 13
US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/819,825
;       FILING DATE:  18-MAR-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lambiris, Elias J.
;       REGISTRATION NUMBER:  33,728
;       REFERENCE/DOCKET NUMBER:  4758.200-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212 867 0123
;       TELEFAX:  212 867 0298
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  467 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-819-825-3

Alignment Scores:
Pred. No.:              4.93e-182       Length:         467
Score:                  1875.00         Matches:        353
Percent Similarity:     84.37%          Conservative:   41
Best Local Similarity:  75.59%          Mismatches:     73
Query Match:            75.60%          Indels:         0
DB:                     2               Gaps:           0

US-09-488-265B-28 (1-1404) x US-08-819-825-3 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              ||||||||||      |||||||||   :::      |||   |||   |||||||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||:::           |||      ||||||||||||||||||   |||||||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||   ||||||||||||||   |||:::|||:::||||||||||:::|||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTGCT 240
              |||   ||||||||:::|||||      ||||||||||||:||   ||||||||||||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||   |||      |||   ||||||||||.||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACCTACAAC 360
              ||||||:::|||||||||   |||   ||||||||||||||||||||||||||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
              |||:::|||||||||||||||||||||||||||||   ::::::||||||||||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
              ||||||||||||:::|||||||||:::|||   |||   |||||||||||||||||:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
              |||||||||   ||||||  |||||||||   :::|||||||||||||||||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
              ||||||   ||||||   :::|||||||   |||:::|||||   |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
              |||   |||      |||||||||||||||   |||:|||||||   |||||||||
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
              |||||||||   |||   |||||||| ||||||||||   |||   |||:::|||||
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
              |||||||||   ||||||   ||||||||||||||||||   :::|||   ||||||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
              ||||||||||   ||||||||||::::   :::::      |||:::|||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
              ||||||   ||||||||||||||||||||||||   ||||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
              ||||||||||||:::|||||||||||||||||||||   ||||||||||||:::|||
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
              ||||||||||||||||||||||||||||||||||||   |||   ||||||:::||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
              ||||||||||||:::|||||||||||||||||||||||||:::|||||||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
              |||||||||   :::||||||||||   |||||||||||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
              ||||||||||||:::|||||||:::|||   :::|||||||||:::|||||||||||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
              ||||||||||||:::|||   ||||||||||||||||||||||||||||:::|||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
              ||||||||||||   |||||   ||||||   ||:||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
              :::|||||||||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 14
US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
;  GENERAL INFORMATION:
;    APPLICANT:  Berka, Randy M.
;    APPLICANT:  Ray, Michael W.
;    APPLICANT:  Klotz, Alan V.
;    TITLE OF INVENTION:  Polypeptides Having Phytase Activity
;    TITLE OF INVENTION:  And Nucleic Acids Encoding Same
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
;      STREET:  405 Lexington Avenue, Suite 6400
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
```

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;      ZIP:  10174-6401
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/163,642
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,825
;      FILING DATE:  18-MAR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lambiris, Elias J.
;      REGISTRATION NUMBER:  33,728
;      REFERENCE/DOCKET NUMBER:  4758.200-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212 867 0123
;      TELEFAX:  212 867 0298
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-163-642-3

Alignment Scores:
Pred. No.:              4.93e-182     Length:        467
Score:                  1875.00       Matches:       353
Percent Similarity:     84.37%        Conservative:  41
Best Local Similarity:  75.59%        Mismatches:    73
Query Match:            75.60%        Indels:        0
DB:                     3             Gaps:          0

US-09-488-265B-28 (1-1404) x US-09-163-642-3 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 240
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        541 AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT 600
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        721 GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG 780
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA 840
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        841 TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT 900
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA 1260
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1261 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG 1320
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 15
US-09-233-510-32
; Sequence 32, Application US/09233510
; Patent No. 6350602
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
```

```
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/233,510
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-233-510-32

Alignment Scores:
Pred. No.:              4.93e-182      Length:          467
Score:                  1875.00        Matches:         353
Percent Similarity:     84.37%         Conservative:    41
Best Local Similarity:  75.59%         Mismatches:      73
Query Match:            75.60%         Indels:          0
DB:                     4              Gaps:            0

US-09-488-265B-28 (1-1404) x US-09-233-510-32 (1-467)

Qy          1 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 60
              ||||.|||||      |||||||||   :::      |||   |||   |||||||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         61 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120
              ||:::            |||      ||||||||||||||||   ||||||||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        121 TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA 180
              |||   |||   ||||||||||||||   |||:::|||:::||||||||||||||:|:|
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        181 TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
              |||   |||||.|||:::||||||      ||||||||||||||   ||||.|||.|||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        241 AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA 300
              ||||||||||||||||||||||||   ||      ||   ||| |||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
                 |||||:::|||||||.|   |||   ||||||||||||:|||||||||||||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT 420
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Qy        421 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCT 480
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Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        481 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 540
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Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

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Qy        601 CCAGAAGGATCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTCGAAGAC 660
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Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTCGCTCCAGCTATTAGA 720
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Qy        901 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT 960
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Qy        961 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1020
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Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1080
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Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1081 CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA 1140
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Qy       1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
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Qy       1381 AACTGGGCTGAATGTTTCGCT 1401
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.1257 Seconds
(without alignments)
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Title: US-09-488-265B-27
Perfect score: 2321
Sequence: 1 NSHSCDTVDGYQCPEISHLW.....DFVEGLSFARSGGNWAECFA 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2020	87.0	441	3	US-09-121-425-1	Sequence 1, Appli
2	2020	87.0	441	4	US-09-634-493A-1	Sequence 1, Appli
3	2020	87.0	467	4	US-09-273-871A-9	Sequence 9, Appli
4	1902	81.9	467	3	US-09-121-425-2	Sequence 2, Appli
5	1902	81.9	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1762.5	75.9	439	4	US-09-044-718-3	Sequence 3, Appli
7	1762.5	75.9	449	4	US-09-044-718-12	Sequence 12, Appl
8	1762.5	75.9	465	3	US-08-868-435-33	Sequence 33, Appl
9	1762.5	75.9	465	4	US-08-744-231-33	Sequence 33, Appl
10	1762.5	75.9	465	4	US-09-044-718-78	Sequence 78, Appl
11	1762.5	75.9	465	4	US-09-636-499-6	Sequence 6, Appli
12	1762.5	75.9	465	4	US-09-273-871A-8	Sequence 8, Appli
13	1754.5	75.6	465	4	US-09-044-718-80	Sequence 80, Appl
14	1753.5	75.5	465	4	US-09-044-718-79	Sequence 79, Appl
15	1750.5	75.4	465	4	US-09-044-718-81	Sequence 81, Appl
16	1707.5	73.6	469	4	US-09-044-718-82	Sequence 82, Appl
17	1688	72.7	466	3	US-08-868-435-12	Sequence 12, Appl
18	1688	72.7	466	4	US-08-744-231-12	Sequence 12, Appl
19	1688	72.7	467	1	US-07-923-724-8	Sequence 8, Appli
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21	1688	72.7	467	2	US-08-374-652C-2	Sequence 2, Appli
22	1684	72.6	444	4	US-09-044-718-1	Sequence 1, Appli
23	1684	72.6	467	1	US-08-151-574-32	Sequence 32, Appl
24	1684	72.6	467	1	US-08-146-424-20	Sequence 20, Appl
25	1684	72.6	467	1	US-08-693-709-2	Sequence 2, Appli
26	1684	72.6	467	2	US-08-419-448-32	Sequence 32, Appl
27	1684	72.6	467	2	US-08-819-825-3	Sequence 3, Appli
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29	1684	72.6	467	4	US-09-233-510-32	Sequence 32, Appl
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36	1672	72.0	443	4	US-09-543-744-1	Sequence 1, Appli
37	1672	72.0	443	4	US-09-929-060-1	Sequence 1, Appli
38	1672	72.0	467	3	US-09-155-855-3	Sequence 3, Appli
39	1672	72.0	467	4	US-09-543-744-3	Sequence 3, Appli
40	1672	72.0	467	4	US-09-273-871A-11	Sequence 11, Appl
41	1672	72.0	467	4	US-09-929-060-3	Sequence 3, Appli
42	1667	71.8	443	3	US-09-155-855-2	Sequence 2, Appli
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45	1660	71.5	462	4	US-09-636-499-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

Query Match 87.0%; Score 2020; DB 3; Length 441;
Best Local Similarity 89.3%; Pred. No. 3.1e-207;
Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 10;

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Db         61 PTSSKSKAYSALIEAIQKNATAPKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

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RESULT 2
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-1

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  Matches  400;  Conservative   10;  Mismatches   20;  Indels   18;  Gaps   10;

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RESULT 3
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; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
;  APPLICANT:  Svendsen, Allan
;  TITLE OF INVENTION:  Phytase Variants
;  FILE REFERENCE:  5618.500-US
;  CURRENT APPLICATION NUMBER: US/09/273,871A
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER:  PA 1998 00407
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  PA 1998 00806
;  PRIOR FILING DATE:  1998-06-19
;  PRIOR APPLICATION NUMBER:  PA 1998 01176
;  PRIOR FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  PA 1999 00091
;  PRIOR FILING DATE:  1999-01-22
;  PRIOR APPLICATION NUMBER:  60/080,129
;  PRIOR FILING DATE:  1998-03-31
;  PRIOR APPLICATION NUMBER:  60/090,675
;  PRIOR FILING DATE:  1998-06-25
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 9
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Variation
US-09-273-871A-9

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RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
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;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2

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Db         87 PTSSKSKAYSA------------------TYNYTLGADDLTPFGENQMVNSGIKFYRRY 127

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVIN---------- 165
              ||||| ||||:|||||||||||||||||||||||||||:    |||||||:
Db        128 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDLIEAIQKNAT 187

Qy        166 ----------VIIPEGSGYNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-L 214
                       |||||||||||||||| ||||||| |||| |:|||||:|:| |'||||||
Db        188 AFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADL 247

Qy        215 PGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGA 272
              ||| |||||||  |||||||:|||||||||:||||| ||| '|| ||| |||, ||||||
Db        248 PGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGA 307

Qy        273 GNPLGPAQGVGF-NELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVS 331
              |||||||||||  |||:|||| ||||||||||||||||||| ||||||||||||||||: :|
Db        308 GNPLGPAQGVGFANELIARLTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMIS 367

Qy        332 IFFALGLYNGTKPLSTTSVESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEP 390
              |||||||||:|| |||||||||| |||||:||||||| ||||||||||:|         ||||
Db        368 IFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQA-------EKEP 420

Qy        391 LVRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 437
              |||||||||||||||| |||||||| ||||||||||||||||||,||
Db        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467


RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-2

  Query Match            81.9%;  Score 1902;  DB 4;  Length 467;
  Best Local Similarity  81.8%;  Pred. No. 1.4e-194;
  Matches  382;  Conservative   10;  Mismatches   19;  Indels   56;  Gaps   11;

Qy          1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
              ||||||||| |||| ||:|||||||||:||| |||||||||  ||||||||||||||||
Db         27 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 86

Qy         59 PTSSKSKKYSALIERIQKNATFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||||| |||                    |||||||||||||||||||||||||||||
Db         87 PTSSKSKAYSA------------------TYNYTLGADDLTPFGENQMVNSGIKFYRRY 127

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADPA---HQASPVIN---------- 165
              ||||| ||||:|||||||||||||||||||||||||||:    |||||||:
Db        128 KALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDLIEAIQKNAT 187

Qy        166 ----------VIIPEGSGYNNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-L 214
                       |||||||||||||||| ||||||| |||| |:|||||:|:| |||||||
Db        188 AFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADL 247

Qy        215 PGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGA 272
              ||| |||||||  |||||||:|||||||||:||||| ||| ||| |||, |||||||
Db        248 PGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGA 307

Qy        273 GNPLGPAQGVGF-NELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVS 331
              |||||||||||  |||:|||| ||||||||||||||||||| ||||||||||||||||: :|
Db        308 GNPLGPAQGVGFANELIARLTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMIS 367

Qy        332 IFFALGLYNGTKPLSTTSVESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEP 390
              |||||||||:|| |||||||||| |||||:||||||| ||||||||||:|         ||||
Db        368 IFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQA-------EKEP 420

Qy        391 LVRVLVNDRVVPLHGCGVDKLGRCKLDDFVEGLSFARSGGNWAECFA 437
              |||||||||||||||| |||||||| ||||||||||||||||||,||
Db        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467


RESULT 6
US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-3

  Query Match            75.9%;  Score 1762.5;  DB 4;  Length 439;
  Best Local Similarity  77.4%;  Pred. No. 1.1e-179;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;
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Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
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Db          1 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 60

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||:|||  |:  || ||| ||||:|||||||||||||.|||||| |:|||||||:|| |
Db         61 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 120

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||| |||||||| ||||||   ::|:| |:|||||   :|| |
Db        121 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 180

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              |||||:|| || | |||:  :||||:||| |||| |  |||| ||||||:|||:| |||
Db        181 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 240

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              |||||||:|||||| ||| :|| :|:|||||:|||||||||||:|| :|||||:|
Db        241 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 300

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
              |||||||||| || ||||||:||:| :|||||:|||||||||||:|| :|||||:|
Db        301 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 360

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
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Db        361 AKELDGYSASWVVPFGARAYFEIMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 413

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
              |||||:|||:|||:|||||| |||:
Db        414 GRCKLNDFVKGLSWARSGGNWGECFS 439


RESULT 7
US-09-044-718-12
; Sequence 12, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-12

  Query Match           75.9%;  Score 1762.5;  DB 4;  Length 449;
  Best Local Similarity  77.4%;  Pred. No. 1.1e-179;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | |||||| |||| |  ||||||||||||| || ::|  :|| ||:| ||||||||||| |
Db         11 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 70

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||||||  |:  || ||| ||||:|||||||||||||||||| |:|||||.|:|| |
Db         71 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 130

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||| ||||||| ||||||   ::|:| |:|||||   :|| |
Db        131 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 190

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              |||||:|| || | |||:  :||||:||| |||| |  |||| ||||||:|||:| |||
Db        191 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 250

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              |||||||:|||||| ||| :|| :|:|||||:|||||||||||:|| :|||||:|
Db        251 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 310

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
              |||||||||| || ||||||:||:| :|||||:|||||||||||:|| :|||||:|
Db        311 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 370

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
                | |||:||| ||| |||| | |||::       ||||:|| |:||||:|||| :|||
Db        371 AKELDGYSASWVVPFGARAYFEIMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 423

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
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Db        424 GRCKLNDFVKGLSWARSGGNWGECFS 449


RESULT 8
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
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;       LOCATION:  205
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  228
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  337
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  374
;       OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33

  Query Match             75.9%;  Score 1762.5;  DB 3;  Length 465;
  Best Local Similarity   77.4%;  Pred. No. 1.2e-179;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | ||||||  |||| |  ||||||||||||||| || ::|  :|| ||:| ||||||||||||
Db         27 SKSCDIVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||||||  |:  || ||| |||||||||||||||||||||| |:|||||||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||| |||||||| ||||||   ::|:| |:||||   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              |||||:|| || | |||:  ||||||||: |||| |||| |||||||:|||||  :|
Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              |||||||:|||||| || :|| :|:|||| |||||||||||||||||:|| ||||||.|
Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
              ||||||||||| || ||||||||||:| ||||||:|||||||||||||||:||| ||| |
Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
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Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
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Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 9
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33

  Query Match             75.9%;  Score 1762.5;  DB 4;  Length 465;
  Best Local Similarity   77.4%;  Pred. No. 1.2e-179;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | ||||||  |||| |  ||||||||||||||| || ::|  :|| ||:| ||||||||||||
Db         27 SKSCDIVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||||||  |:  || ||| |||||||||||||||||||||| |:|||||||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||| |||||||| ||||||   ::|:| |:||||   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              |||||:|| || | |||:  ||||||||: |||| |||| |||||||:|||||  :|
Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              |||||||:|||||| || :|| :|:|||| |||||||||||||||||:|| ||||||.|
Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
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Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
              | |||:||| ||| |||| | |||::       ||||||| |:||||||||||| ||||
Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
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Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 10
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 78
;  LENGTH: 465
;  TYPE: PRT
;  ORGANISM: Aspergillus fumigatus
US-09-044-718-78

  Query Match             75.9%;  Score 1762.5;  DB 4;  Length 465;
  Best Local Similarity   77.4%;  Pred. No. 1.2e-179;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
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Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
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Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||| |||||||| ||||||   ::|:| |:||||   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              ||||||| ||  | |||:  |||||:||| |||| |  |||| |||||||:|||| |||
Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
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Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSITSVES 352
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Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRISVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
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Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
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Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 11
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
;  APPLICANT:  Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION:  Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE:  GC586-2
;  CURRENT APPLICATION NUMBER: US/09/636,499
;  CURRENT FILING DATE:  2000-08-11
;  PRIOR APPLICATION NUMBER:  US 60/148,960
;  PRIOR FILING DATE:  1999-08-13
;  NUMBER OF SEQ ID NOS:  34
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;  LENGTH: 465
;  TYPE: PRT
;  ORGANISM: Aspergillus fumigatus
US-09-636-499-6

  Query Match             75.9%;  Score 1762.5;  DB 4;  Length 465;
  Best Local Similarity   77.4%;  Pred. No. 1.2e-179;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
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Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              |||||||| |:  || ||| |:||:|:|||||,|||||||||| |:||||||||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||| |||||||| ||||||   ::|:| |:||||   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
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Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
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Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSITSVES 352
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Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRISVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
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Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
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Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 12
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
;  APPLICANT:  Svendsen, Allan
;  TITLE OF INVENTION:  Phytase Variants
;  FILE REFERENCE:  5618.500-US
;  CURRENT APPLICATION NUMBER: US/09/273,871A
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER:  PA 1998 00407
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  PA 1998 00806
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;  PRIOR FILING DATE:  1998-06-19
;  PRIOR APPLICATION NUMBER:  PA 1998 01176
;  PRIOR FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  PA 1999 00091
;  PRIOR FILING DATE:  1999-01-22
;  PRIOR APPLICATION NUMBER:  60/080,129
;  PRIOR FILING DATE:  1998-03-31
;  PRIOR APPLICATION NUMBER:  60/090,675
;  PRIOR FILING DATE:  1998-06-25
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-273-871A-8

  Query Match             75.9%;  Score 1762.5;  DB 4;  Length 465;
  Best Local Similarity   77.4%;  Pred. No. 1.2e-179;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | ||||||  |||| |  ||||||||||||| || ::|  :|| ||:| ||||||||||||
Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRIILVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||||||  |:  || ||| |||:|||||||||||||||||||| |:|||||||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||| |||||||| ||||||   ::|:| |:||| |   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
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Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
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Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTISVES 352
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Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
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Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
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Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 13
US-09-044-718-80
; Sequence 80, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-80

  Query Match             75.6%;  Score 1754.5;  DB 4;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 8.4e-179;
  Matches  344;  Conservative   36;  Mismatches   49;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | ||||||  |||| |  ||||||||||||| || ::|  :|| ||:| ||||||||||||
Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||||||  |:  || ||| |||:|||||||||||||||||||| |:|||||||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
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Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
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Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
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Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTISVES 352
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Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
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Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
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RESULT 14
US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-79

  Query Match             75.5%;  Score 1753.5;  DB 4;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 1.1e-178;
  Matches  344;  Conservative   36;  Mismatches   49;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
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Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118

Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176

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Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235

Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

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Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411

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Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437

Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 15
US-09-044-718-81
; Sequence 81, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-81

  Query Match             75.4%;  Score 1750.5;  DB 4;  Length 465;
  Best Local Similarity   76.9%;  Pred. No. 2.3e-178;
  Matches  343;  Conservative   37;  Mismatches   49;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVIFVQVLSRHGARYP 59

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Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118

Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTAFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176

Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235

Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAKKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292

Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352

Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411

Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437

Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465


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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 ; Search time 99.8585 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-27
Perfect score: 2321
Sequence: 1 NSHSCDTVDGYQCPEISHLW.....DFVEGLSFARSGGNWAECFA 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2020	87.0	467	14	US-10-083-452-9	Sequence 9, Appli
2	1762.5	75.9	439	15	US-10-062-848-3	Sequence 3, Appli
3	1762.5	75.9	449	15	US-10-062-848-12	Sequence 12, Appl
4	1762.5	75.9	465	14	US-10-083-452-8	Sequence 8, Appli
5	1762.5	75.9	465	15	US-10-062-848-78	Sequence 78, Appl
6	1762.5	75.9	465	15	US-10-229-358-6	Sequence 6, Appli
7	1762.5	75.9	474	15	US-10-213-990-24	Sequence 24, Appl
8	1754.5	75.6	465	15	US-10-062-848-80	Sequence 80, Appl
9	1753.5	75.5	465	15	US-10-062-848-79	Sequence 79, Appl
10	1750.5	75.4	465	15	US-10-062-848-81	Sequence 81, Appl
11	1707.5	73.6	469	15	US-10-062-848-82	Sequence 82, Appl
12	1684	72.6	444	15	US-10-062-848-1	Sequence 1, Appli
13	1684	72.6	467	15	US-10-079-709-32	Sequence 32, Appl
14	1684	72.6	467	15	US-10-229-358-5	Sequence 5, Appli
15	1676.5	72.2	447	15	US-10-062-848-6	Sequence 6, Appli
16	1676.5	72.2	463	14	US-10-083-452-10	Sequence 10, Appl
17	1672	72.0	443	9	US-09-929-060-1	Sequence 1, Appli
18	1672	72.0	467	9	US-09-929-060-3	Sequence 3, Appli
19	1672	72.0	467	14	US-10-083-452-11	Sequence 11, Appl
20	1667	71.8	443	9	US-09-929-060-2	Sequence 2, Appli
21	1660	71.5	462	15	US-10-229-358-12	Sequence 12, Appl
22	1596.5	68.8	450	15	US-10-062-848-9	Sequence 9, Appli
23	1596.5	68.8	466	14	US-10-083-452-13	Sequence 13, Appl
24	1589	68.5	438	15	US-10-062-848-2	Sequence 2, Appli
25	1588	68.4	450	15	US-10-062-848-15	Sequence 15, Appl
26	1562.5	67.3	466	14	US-10-083-452-12	Sequence 12, Appl
27	1562.5	67.3	466	15	US-10-229-358-7	Sequence 7, Appli
28	1519	65.4	489	15	US-10-229-358-4	Sequence 4, Appli
29	1519	65.4	489	15	US-10-229-358-10	Sequence 10, Appl
30	1470	63.3	410	15	US-10-229-358-11	Sequence 11, Appl
31	1322	57.0	475	14	US-10-083-452-14	Sequence 14, Appl
32	1275.5	55.0	487	14	US-10-083-452-15	Sequence 15, Appl
33	1275.5	55.0	487	15	US-10-229-358-8	Sequence 8, Appli
34	1230.5	53.0	355	15	US-10-229-358-15	Sequence 15, Appl
35	1185	51.1	478	14	US-10-083-452-3	Sequence 3, Appli
36	1185	51.1	495	14	US-10-083-452-2	Sequence 2, Appli
37	841	36.2	284	15	US-10-229-358-19	Sequence 19, Appl
38	837.5	36.1	443	14	US-10-083-452-5	Sequence 5, Appli
39	825	35.5	283	15	US-10-229-358-9	Sequence 9, Appli
40	825	35.5	283	15	US-10-229-358-24	Sequence 24, Appl
41	812.5	35.0	453	14	US-10-083-452-6	Sequence 6, Appli
42	804.5	34.7	439	14	US-10-083-452-7	Sequence 7, Appli
43	793	34.2	442	14	US-10-083-452-4	Sequence 4, Appli
44	663	28.6	212	15	US-10-229-358-16	Sequence 16, Appl
45	372.5	16.0	312	15	US-10-229-358-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 87.0%; Score 2020; DB 14; Length 467;
Best Local Similarity 89.3%; Pred. No. 6.3e-197;
Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 10;

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RESULT 6
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-229-358-6

  Query Match             75.9%;  Score 1762.5;  DB 15;  Length 465;
  Best Local Similarity   77.4%;  Pred. No. 1.1e-170;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
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Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||||||  ||:  || ||| |||||||||||||||||||||| |:||||||||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||||| |||||||| ||||||   ::|:| |:|:|||   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              |||||:|| || | |||:  |||||:||| |||| |  |||| |||||||:|||| |||
Db        207 TLDHGVCIKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              |||||||:|||||| ||| :|| :|:|||| ||||||||||||||:|| ||||:|||
Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSITSVES 352
              |||||||||| || |||||||||||:| ||||||:|||||||||||||:||| |||||
Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
              | |||:||| ||| |||| | |||::       |:|||||  |:|||||||||| ||||
Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
              |||||:|||:|||:|||||| |||:
Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 7
US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Bo
;  APPLICANT:  Bussey, Howard
;  APPLICANT:  Storms, Reg
;  APPLICANT:  Roemer, Terry
;  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
;  TITLE OF INVENTION:  ENZYMES AND METHODS OF USE
;  FILE REFERENCE: 10182-019-999
;  CURRENT APPLICATION NUMBER: US/10/213,990
;  CURRENT FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Aspergillus
US-10-213-990-24

  Query Match             75.9%;  Score 1762.5;  DB 15;  Length 474;
  Best Local Similarity   77.4%;  Pred. No. 1.1e-170;
  Matches  345;  Conservative   36;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | ||||||  |||  |  ||||||||||||| || ::|  :|| ||:| ||||||||||
Db         36 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 95

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              ||||||||  ||:  || ||| |||||||||||||||||||||| |:||||||||:||
Db         96 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 155

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||||| |||||||| ||||||   ::|:| |:|:|||   :||
Db        156 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 215

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              |||||:|| || | |||:  |||||:||| |||| |  |||| |||||||:|||| |||
Db        216 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 275

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              |||||||:|||||| ||| :|| :|:|||| ||||||||||||||:|| ||||:|||
Db        276 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 335

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSITSVES 352
              |||||||||| || |||||||||||:| ||||||:|||||||||||||:||| |||||
Db        336 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 395

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
              | |||:||| ||| |||| | |||::       |:|||||  |:|||||||||| ||||
Db        396 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 448

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
              |||||:|||:|||:|||||| |||:
Db        449 GRCKLNDFVKGLSWARSGGNWGECFS 474


RESULT 8
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
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US-10-062-848-80

Query Match 75.6%; Score 1754.5; DB 15; Length 465;
Best Local Similarity 77.1%; Pred. No. 7.2e-170;
Matches 344; Conservative 36; Mismatches 49; Indels 17; Gaps 10;

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Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | |||||| |||| | ||||||||||||| || ::| :|| ||:| ||||:|||||||
Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              |||||||  |:  || ||| ||||:|||||||||||||||||||| |:|||:|||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||||| |||||||| ||||||   ::|:| |:|||||   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              ||||||:|| || | |||:  |||||:||| |||| |  |||| :|||||||:|||| ||
Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
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Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
              |||||||||| || |||||||||:| ||||||:||||||||||||||:||| ||:||
Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
                | |||:||| ||| |||| ! |||::       ||| ||| |:|||||||||| ||||
Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKESLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
              |||||:|||:|||:|||||:| |||:
Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465
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RESULT 9
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Query Match 75.5%; Score 1753.5; DB 15; Length 465;
Best Local Similarity 77.1%; Pred. No. 9.1e-170;
Matches 344; Conservative 36; Mismatches 49; Indels 17; Gaps 10;

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Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
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Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              |||||||  |:  || ||| ||||:|||||||||||||||||||| |:|||:|||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||||| |||||||| ||||||   ::|:| |:|||||   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              ||||||:|| || | |||:  |||||:||| |||| |  |||| :|||||||:|||| ||
Db        207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              |||||||:|||||| ||| :|| :|:|||| ||||||||||||||||:|| ||||||||
Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
              |||||||||| || |||||||||:| ||||||:||||||||||||||:||| ||:||
Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy        353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
                | |||:||| ||| |||| ! |||::       ||| ||| |:|||||||||| ||||
Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKESLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
              |||||:|||:|||:|||||:| |||:
Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465
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Qy 60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
Db 87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 146

Qy 119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
Db 147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206

Qy 177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
Db 207 TLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFDT 266

Qy 236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
Db 267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
Db 327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy 353 I-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
Db 387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKESLVRALINDRVVPLHGCDVDKL 439

Qy 412 GRCKLDDFVEGLSFARSGGNWAECFA 437
Db 440 GRCKLNDFVKGLSWARSGGNWGECFS 465

RESULT 10
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 75.4%; Score 1750.5; DB 15; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.8e-169;
Matches 343; Conservative 37; Mismatches 49; Indels 17; Gaps 10;

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Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | |||||| |||| | ||||||||||||| || ::| :|| ||:| ||||||||||||
Db         27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              |||||||  |:  || ||| ||||:|||||||||||||||||||| ||| |:|||||:||
Db         87 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTAFGEQQLVNSGIKFYQRY 146

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||||::|||:|||||||||||| |||||||| ||||||   ::|:| |:|||||   :||
Db        147 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGATNRAAPAISVIIPESETFNN 206
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Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              ||||:|| || | |||:  |||||:||| |||| :  |||| |||||||:||||| |||
Db        207 TLDHGVCTKFFASQLGDEVAANFTALFAPDIRARAKKHLPGVILTDEDVVSLMDMCSFDT 266

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              ||||||:||||:| ||| :| :|:||||| ||||||||||:||||||:|| |||||||
Db        267 VARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 326

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
               ||||||||| || |||||||||||:| ||:|||:||||||||||||||||:||| ||| |
Db        327 RSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVES 386

Qy        353 I-ETDGYAASWTVPFFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
                | |||:||| ||| |||| | |||::        |||||| |:|:|||.|||| ||||
Db        387 AKELDGYSASWVVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCDVDKL 439

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
              |||||:|||:|||:|:||||| |||:
Db        440 GRCKLNDFVKGLSWARSGGNWGECFS 465
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RESULT 11
US-10-062-848-82
; Sequence 82, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 469
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-82

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  Query Match             73.6%;  Score 1707.5;  DB 15;  Length 469;
  Best Local Similarity   74.4%;  Pred. No. 4.5e-165;
  Matches  332;  Conservative   49;  Mismatches   48;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              | :||||: |||| |  |||||||||||| || ::| |:|| |||||||||||||||||
Db         31 SKACDTVELGYQCSPGTSHLWGQYSPFFSLEDELSVSSDLPKDCRVTFVQVLSRHGARYP 90

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              |:|||||| |:  |||||:||||:|||||||||||||||||||| |||:||||||::|
Db         91 TASKSKKYKKLVTAIQKNATEFKGKFAFLETYNYTLGADDLTPFGEQQMVNSGIKFYQKY 150

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP--AHQASPVINVIIPEGSGYNN 176
              |||| ::|||:|:||||||||| |||||||| | :|||    ::|:|||:||||  |:|
Db        151 KALAGSVVPFIRSSGSDRVIASGEKFIEGFQQANVADPGATNRAAPVISVIIPESETYNN 210

Qy        177 TLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLEA-LPGVNLTDEDVVNLMDMCPFDT 235
              |||| :|| || | |||: ||||||:||| ||||:|  |||| |||:|||:||||| |:|
Db        211 TLDHSVCTNFEASELGDEVEANFTALFAPAIRARIEKHLPGVQLTDDDVVSLMDMCSFDT 270

Qy        236 VARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
              ||||:||::||||| :||  :|| :|||||| |||||||||||||||:|| ||||||||
Db        271 VARTADASELSPFCAIFTHNEWKKYDYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARLT 330

Qy        293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
              :||||||||||| |||:|||||||||:|||||||:|:|||||:||||||||||:|||| ||
Db        331 NSPVQDHTSTNSTLDSDPATFPLNATIYVDFSHDNGMIPIFFAMGLYNGTEPLSQTSEES 390

Qy        353 I-ETDGYAASWTVPFFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKL 411
              |::||:||| ||| |||| | |||::        |||||| |:||||||||||| ||||
Db        391 TKESNGYSASWAVPFGARAYFETMQCKS-------EKEPLVRALINDRVVPLHGCAVDKL 443

Qy        412 GRCKLDDFVEGLSFARSGGNWAECFA 437
              ||||| |||:|||:||||||  : |:
Db        444 GRCKLKDFVKGLSWARSGGNSEQSFS 469
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RESULT 12
US-10-062-848-1
; Sequence 1, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-062-848-1

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  Query Match             72.6%;  Score 1684;  DB 15;  Length 444;
  Best Local Similarity   73.9%;  Pred. No. 1e-162;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   18;  Gaps   10;

Qy          1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
              | ||||| ||||  | |||||:||||||:|| |||:|| |||||| ||||||||
Db          4 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 63

Qy         59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
              || || |||||||| ||:|| || |||||||||||:|||||||||| ::||:||||:|
Db         64 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 123

Qy        118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
              |::| ||||||:|:||| ||||| :||||||| || ||      |:|| |:|:| | |
Db        124 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 183

Qy        175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
              |||| | || |||| | | |||||| | | || |||  | || |||  :|  |||||| |
Db        184 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 243

Qy        234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
              |:: :: |:||||||||| |||  ||||||| ||||:|||||||:| ||||: ||||||
Db        244 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 303

Qy        291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
              |||||| | ||:||||||:||||||:||||||||||| :::| ||||||||||||||:|
Db        304 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTV 363

Qy        351 ESI-ETDGYAASWTVPFFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
              |:| :|||::::|||||:| |||||||:|         |:|||||||||||||||||| ||
Db        364 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 416

Qy        410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
              ||||  | || |||||||||:||||||
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Db        417 ALGRCTRDSFVRGLSFARSGGDWAECFA 444


RESULT 13
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
;  GENERAL INFORMATION:
;    APPLICANT:  Robert F.M. Van Gorcom
;    APPLICANT:  Willem Van Hartingsveldt
;    APPLICANT:  Petrus A. Van Paridon
;    APPLICANT:  Annemarie E. Veenstra
;    APPLICANT:  Rudolf G.M. Luttin
;    APPLICANT:  Gerardus Selten
;    TITLE OF INVENTION:  Cloning and Expression of Microbial
;    TITLE OF INVENTION:  Phytase
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  545 Middlefield Road, Suite 200
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025-3471
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      SOFTWARE:
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/079,709
;      FILING DATE:  02-FEB-2002
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/233,510
;      FILING DATE:  20-JAN-1999
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-079-709-32

  Query Match             72.6%;  Score 1684;  DB 15;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 1.1e-162;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   16;  Gaps   10;

Qy          1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
              |  |||||| |:||  | ||||||:||||:|:|| |||:|| |||||| ||||:|||||
Db         27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86

Qy         59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
              || || |||||||| ||:|| || ||||||||||:|||||||||| ::|||||||:|
Db         87 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy        118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
              |::| ||||||:|:||| ||||| :|||||||| || ||     |:|| |:|:| | |
Db        147 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy        175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
              ||||| | || |||| : |  |||||| | | || |||  | || ||| :|  ||||| |
Db        207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy        234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
              ||:: ::  |:|||||||| |||  ||||||| ||||:|||||| |||: ||||||
Db        267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy        291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
              |||||| | ||:|||||:||||||':|||||||||| ::|| ||||||||||||||:|
Db        327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTITV 386

Qy        351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
              |:| :|||:::::|||||:| |||||||:|       |:|||||||||||||||| ||
Db        387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 439

Qy        410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
              ||||  | || ||||||||||:||||||
Db        440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 14
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Irinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-229-358-5

  Query Match             72.6%;  Score 1684;  DB 15;  Length 467;
  Best Local Similarity   73.9%;  Pred. No. 1.1e-162;
  Matches  331;  Conservative   40;  Mismatches   59;  Indels   16;  Gaps   10;

Qy          1 NSHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 58
              |  |||||| |:||  | ||||||:||||:|:|| |||:|| |||||| ||||:|||||
Db         27 NQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARY 86

Qy         59 PTSSKSKKYSALIERIQKNA-TFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 117
              || || |||||||| ||:|| || ||||||||||:|||||||||| ::|||||||:|
Db         87 PTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQR 146

Qy        118 YKALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLADP---AHQASPVINVIIPEGSGY 174
              |::| ||||||:|:||| ||||| :|||||||| || ||     |:|| |:|:| | |
Db        147 YESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSS 206

Qy        175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLTDEDVVNLMDMCPF 233
              ||||| | || |||| : |  |||||| | | || |||  | || ||| :|  ||||| |
Db        207 NNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSF 266

Qy        234 DTVARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
              ||:: ::  |:|||||||| |||  ||||||| ||||:|||||| |||: ||||||
Db        267 DTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR 326

Qy        291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 350
              |||||| | ||:|||||:||||||':|||||||||| ::|| ||||||||||||||:|
Db        327 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTITV 386

Qy        351 ESI-ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVD 409
              |:| :|||:::::|||||:| |||||||:|       |:|||||||||||||||| ||
Db        387 ENITQTDGFSSAWTVPFASRLYVEMMQCQA-------EQEPLVRVLVNDRVVPLHGCPVD 439
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Qy        410 KLGRCKLDDFVEGLSFARSGGNWAECFA 437
              ||||  | || |||||||||:|||||||
Db        440 ALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 15
US-10-062-848-6
; Sequence 6, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Aspergillus nidulans
US-10-062-848-6

  Query Match             72.2%;  Score 1676.5;  DB 15;  Length 447;
  Best Local Similarity   73.4%;  Pred. No. 6.1e-162;
  Matches  326;  Conservative   43;  Mismatches   58;  Indels   17;  Gaps   10;

Qy          2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 59
              :|||:| | |||| : :||:|||||:|:||:  ||||| ||| || ||||||||||||||
Db         10 NHSCNTADGGYQCFPNVSHVWGQYSPYFSIEQESAISEDVPHGCEVTFVQVLSRHGARYP 69

Qy         60 TSSKSKKYSALIERIQKNAT-FKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRRY 118
              | |||| || ||| |||||| | |:|||||:|||||||||||| ||||||||:|| ||||||
Db         70 TESKSKAYSGLIEAIQKNATSFWGQYAFLESYNYTLGADDLTIFGENQMVDSGAKFYRRY 129

Qy        119 KALARNIVPFVRASGSDRVIASAEKFIEGFQSAKLAD-PAHQASPVINVIIPEGSGYNNT 177
              | |||   ||:|||||||||:|||||| ||: |:| |  : :|:||:|||||  |:|||
Db        130 KNLARKNTPFIRASGSDRVVASAEKFINGFRKAQLHDHGSKRATPVVNVIIPEIDGFNNI 189

Qy        178 LDHGLCTAFEDSTLGDDAEANFTAVFAPPIRARLE-ALPGVNLIDEDVVNLMDMCPFDTV 236
              ||| | :||:    |: ||||||:  |||| ||| |||: ||:|:|: ||||| |||:
Db        190 LDHSTCVSFENDERADEIEANFTAIMGPPIRKRLENDLPGIKLTNENVIYLMDMCSFDTM 249

Qy        237 ARTSDATQLSPFCDLFTADEW-QYDYLQSL-KYYGYGAGNPLGPAQGVGF-NELIARLTH 293
              |||:  |:|||| :||  || |||||||| |||||||:||||||||:|| ||||'||
Db        250 ARTAHGTELSPFCAIFTEKEWLQYDYLQSLSKYYGYGAGSPLGPAQGIGFTNELIARLTQ 309

Qy        294 SPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTISVESI 353
              |||||:|||||||||||||'||:  ||||||||||:|:|||||:||||||:|||  ||||!
Db        310 SPVQDNTSTNHTLDSNPATFPLDRKLYADFSHDNSMISIFFAMGLYNGTQPLSMDSVESI 369

Qy        354 -ETDGYAASWTVPFAARAYVEMMQCEAGGGGGEGEKEPLVRVLVNDRVVPLHGCGVDKLG 412
               | |||||||||||| |||| |:||||         :|||||)||||||||||| | |:: |
Db        370 QEMDGYAASWTVPFGARAYFELMQCE--------KKEPLVRVLVNDRVVPLHGCAVDKFG 421

Qy        413 RCKLDDFVEGLSFARSGGNWAECF 436
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Db        422 RCTLDDWVEGLNFARSGGNWKTCF 445


Search completed: October  3, 2003, 08:12:29
Job time : 100.859 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 ; Search time 106.714 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-26
Perfect score: 2470
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWEECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2311	93.6	467	14	US-10-083-452-9	Sequence 9, Appli
2	1902	77.0	465	14	US-10-083-452-8	Sequence 8, Appli
3	1902	77.0	465	15	US-10-062-848-78	Sequence 78, Appl
4	1902	77.0	465	15	US-10-229-358-6	Sequence 6, Appli
5	1895.5	76.7	474	15	US-10-213-990-24	Sequence 24, Appl
6	1894	76.7	465	15	US-10-062-848-80	Sequence 80, Appl
7	1893	76.6	465	15	US-10-062-848-79	Sequence 79, Appl
8	1892.5	76.6	439	15	US-10-062-848-3	Sequence 3, Appli
9	1892.5	76.6	449	15	US-10-062-848-12	Sequence 12, Appl
10	1890	76.5	465	15	US-10-062-848-81	Sequence 81, Appl
11	1868	75.6	469	15	US-10-062-848-82	Sequence 82, Appl
12	1862	75.4	467	15	US-10-079-709-32	Sequence 32, Appl
13	1862	75.4	467	15	US-10-229-358-5	Sequence 5, Appli
14	1855	75.1	467	9	US-09-929-060-3	Sequence 3, Appli
15	1850	74.9	467	14	US-10-083-452-11	Sequence 11, Appl
16	1843	74.6	462	15	US-10-229-358-12	Sequence 12, Appl
17	1820	73.7	444	15	US-10-062-848-1	Sequence 1, Appli
18	1813.5	73.4	463	14	US-10-083-452-10	Sequence 10, Appl
19	1813	73.4	443	9	US-09-929-060-1	Sequence 1, Appli
20	1808	73.2	443	9	US-09-929-060-2	Sequence 2, Appli
21	1798.5	72.8	447	15	US-10-062-848-6	Sequence 6, Appli
22	1756	71.1	466	14	US-10-083-452-12	Sequence 12, Appl
23	1756	71.1	466	15	US-10-229-358-7	Sequence 7, Appli
24	1752	70.9	450	15	US-10-062-848-15	Sequence 15, Appl
25	1719	69.6	466	14	US-10-083-452-13	Sequence 13, Appl
26	1715.5	69.5	450	15	US-10-062-848-9	Sequence 9, Appli
27	1701	68.9	438	15	US-10-062-848-2	Sequence 2, Appli
28	1661	67.2	489	15	US-10-229-358-4	Sequence 4, Appli
29	1661	67.2	489	15	US-10-229-358-10	Sequence 10, Appl
30	1637	66.3	410	15	US-10-229-358-11	Sequence 11, Appl
31	1395	56.5	475	14	US-10-083-452-14	Sequence 14, Appl
32	1346.5	54.5	487	14	US-10-083-452-15	Sequence 15, Appl
33	1346.5	54.5	487	15	US-10-229-358-8	Sequence 8, Appli
34	1335	54.0	355	15	US-10-229-358-15	Sequence 15, Appl
35	1222	49.5	495	14	US-10-083-452-2	Sequence 2, Appli
36	1217	49.3	478	14	US-10-083-452-3	Sequence 3, Appli
37	917	37.1	284	15	US-10-229-358-19	Sequence 19, Appl
38	880	35.6	283	15	US-10-229-358-9	Sequence 9, Appli
39	880	35.6	283	15	US-10-229-358-24	Sequence 24, Appl
40	846.5	34.3	443	14	US-10-083-452-5	Sequence 5, Appli
41	833.5	33.7	453	14	US-10-083-452-6	Sequence 6, Appli
42	831.5	33.7	439	14	US-10-083-452-7	Sequence 7, Appli
43	822	33.3	442	14	US-10-083-452-4	Sequence 4, Appli
44	729.5	29.5	212	15	US-10-229-358-16	Sequence 16, Appl
45	412	16.7	312	15	US-10-229-358-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 93.6%; Score 2311; DB 14; Length 467;
Best Local Similarity 93.1%; Pred. No. 5.9e-225;
Matches 435; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDIVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
Db        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db        181 KLADPGSQPHQASPVIDVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        241 ARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLG 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHISTNHTLDSNPATFPLNATLYADFS 360
Db        301 KYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Qy        361 HDNIMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
Db        361 HDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQAEKEP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467
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RESULT 2
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

Query Match 77.0%; Score 1902; DB 14; Length 465;
Best Local Similarity 77.1%; Pred. No. 1.5e-183;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFINELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
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RESULT 3
US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-78

Query Match 77.0%; Score 1902; DB 15; Length 465;
Best Local Similarity 77.1%; Pred. No. 1.5e-183;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300

Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420

Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467

Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 4
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700Ai
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-229-358-6

  Query Match             77.0%;  Score 1902;  DB 15;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 1.5e-183;
  Matches  360;  Conservative   37;  Mismatches   68;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60

Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120

Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180

Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240

Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300

Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420

Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467

Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 5
US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Bo
;  APPLICANT:  Bussey, Howard
;  APPLICANT:  Storms, Reg
;  APPLICANT:  Roemer, Terry
;  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
;  TITLE OF INVENTION:  ENZYMES AND METHODS OF USE
;  FILE REFERENCE: 10182-019-999
;  CURRENT APPLICATION NUMBER: US/10/213,990
;  CURRENT FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Aspergillus
US-10-213-990-24

  Query Match             76.7%;  Score 1895.5;  DB 15;  Length 474;
  Best Local Similarity   76.4%;  Pred. No. 7e-183;
  Matches  356;  Conservative   42;  Mismatches   61;  Indels    7;  Gaps    2;

Qy          2 GVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADES 61

Db         16 GAVVLILKRSRVSAAPSS------AGSKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDEL 69

Qy         62 AISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNY 121

Db         70 SVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNY 129

Qy        122 TLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSAK 181

Db        130 TLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQAK 189

Qy        182 LADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRA 241

Db        190 LADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIRA 248

Qy        242 RLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGK 301

Db        249 RAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGK 308

Qy        302 YYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSH 361

Db        309 YYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSH 368

Qy        362 DNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPL 421

Db        369 DNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEPL 428

Qy        422 VRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467

Db        429 VRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 474


RESULT 6
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
```

```
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-80

  Query Match             76.7%;  Score 1894;  DB 15;  Length 465;
  Best Local Similarity   76.9%;  Pred. No. 9.7e-183;
  Matches  359;  Conservative   37;  Mismatches   69;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              |     ||| | |        |    | | ||||| |||| |  ||||||||||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                ::|  :|| ||:| ||||:|||||||||||||||  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:|||||||:||||||| :|||:|||||||||| ||||||||  |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :||||||||:|| || |:|||:| ||||||||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:|||| ||||||||||:|||||  ||||:|| :|:|||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:| |||||||| ||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| ||||| :| |||:||| ||| |||| | ||||:|||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKES 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:||||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 7
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-79

  Query Match             76.6%;  Score 1893;  DB 15;  Length 465;
  Best Local Similarity   76.9%;  Pred. No. 1.2e-182;
  Matches  359;  Conservative   37;  Mismatches   69;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              |     ||| | |        |    | | ||||| |||| |  ||||||||||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                ::|  :|| ||:| ||||:|||||||||||||||  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:|||||||:||||||| :|||:|||||||||| ||||||||  |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :||||||||:|| || |:|||:| ||||||||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:|||| ||||||||||:|||||  ||||:|| :|:|||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:| |||||||| ||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| ||||| :| |||:||| ||| |||| | ||||:|||
Db        359 HDNSMVSIFFALGLYNGTEGLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:||||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 8
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
```

US-10-062-848-3

Query Match 76.6%; Score 1892.5; DB 15; Length 439;
Best Local Similarity 80.0%; Pred. No. 1.3e-182;
Matches 352; Conservative 37; Mismatches 50; Indels 1; Gaps 1;

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Qy         28 SHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 87
              | |||||| |||| | |||||||||||||| || ::|  :|| ||:| ||||||||||||
Db          1 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 60

Qy         88 TSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRY 147
              |||||||| |: ||| ||| |||||||||||||||||||||||||||||||||||||||
Db         61 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 120

Qy        148 KALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYN 207
              ||||| ||||||||||||||| |||||||| |||||||  ::|:| |:|||||   :|
Db        121 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGAT-NRAAPAISVIIPESETFN 179

Qy        208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFD 267
              ||||||:|| || |:|||:| |||||:||| |||| | |||| |||||||:|||| ||
Db        180 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFD 239

Qy        268 TVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
              |||||||||:|||||| ||||:|| :|:|||||||||||||||||||||||:|| ||||||
Db        240 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 299

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNIMVSIFFALGLYNGTKPLSTTSVE 387
              | |||||||||| || |||||||||||:| ||||||:|||||||||||||||:||| |||
Db        300 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 359

Qy        388 SIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
              | :| |||:||| ||| |||| | |||::|||||| |:|||||||| |||||||| :
Db        360 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 419

Qy        448 DFVEGLSFARSGGNWEECFA 467
              |||:|||:|||||| |||:
Db        420 DFVKGLSWARSGGNWGECFS 439
```

RESULT 9
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 76.6%; Score 1892.5; DB 15; Length 449;
Best Local Similarity 80.0%; Pred. No. 1.3e-182;
Matches 352; Conservative 37; Mismatches 50; Indels 1; Gaps 1;

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Qy         28 SHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 87
              | |||||| |||| | |||||||||||||| || ::|  :|| ||:| ||||||||||||
Db         11 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 70

Qy         88 TSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRY 147
              |||||||| |: ||| ||| |||||||||||||||||||||||||||||||||||||||
Db         71 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 130

Qy        148 KALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYN 207
              ||||| ||||||||||||||| |||||||| |||||||  ::|:| |:|||||   :|
Db        131 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGAT-NRAAPAISVIIPESETFN 189

Qy        208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFD 267
              ||||||:|| || |:|||:| |||||:||| |||| | |||| |||||||:|||| ||
Db        190 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFD 249

Qy        268 TVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
              |||||||||:|||||| ||||:|| :|:|||||||||||||||||||||||:|| ||||||
Db        250 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 309

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVE 387
              | |||||||||| || |||||||||||:| ||||||:|||||||||||||||:||| |||
Db        310 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 369

Qy        388 SIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
              | :| |||:||| ||| |||| | |||::|||||| |:|||||||| |||||||| :
Db        370 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 429

Qy        448 DFVEGLSFARSGGNWEECFA 467
              |||:|||:|||||| |||:
Db        430 DFVKGLSWARSGGNWGECFS 449
```

RESULT 10
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 76.5%; Score 1890; DB 15; Length 465;
Best Local Similarity 76.7%; Pred. No. 2.5e-182;
Matches 358; Conservative 38; Mismatches 69; Indels 2; Gaps 2;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  ||||||||||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
              ::|  :|| ||:| ||||||||||||||||||  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              ||||||||| ||||||||:||||||| :|||:|||||||||| |||||||| |
Db        120 YTLGADDLTAFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179
```

```
Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              ||||||  ::|:| |::||||    :||:|||:|| || |:|||:| ||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || : ||||| |||||||:||||| ||||||||||:|||||| ||||:|| :|:||||||
Db        239 ARAKKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:|| |||||||| |||||||||| || |||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              |||:||||||||||||||:||| ||||| :| |||:||| |||| |||| | |||::||| 
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:||||||||||| |||||||| :|||:|||:||||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
```

RESULT 11
US-10-062-848-82
; Sequence 82, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
;   LENGTH: 469
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-82

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  Query Match             75.6%;  Score 1868;  DB 15;  Length 469;
  Best Local Similarity   74.0%;  Pred. No. 4.2e-180;
  Matches  348;  Conservative   52;  Mismatches   66;  Indels    4;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSG---TALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSL 57
              ||      |||:  |      :|    :        | :||||: |||| |   |||||||||||
Db          1 MGALTFLLSVMYLLSGVAGAPSSGCSAGSGSKACDTVELGYQCSPGTSHLWGQYSPFFSL 60

Qy         58 ADESAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEATQKNATAFKGKYAFLK 117
               || ::| |:|| ||||||||||||||||||:|||||   |: ||||||| ||||:|||:
Db         61 EDELSVSSDLPKDCRVTFVQVLSRHGARYPTASKSKKYKKLVTAIQKNATEFKGKFAFLE 120

Qy        118 TYNYTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGF 177
              |||||||||||||||||||||||||||:|||||   :|||:|:|||||||:|| ||||||
Db        121 TYNYTLGADDLTPFGEQQMVNSGIKFYQKYKALAGSVVPFIRSSGSDRVIASGEKFIEGF 180

Qy        178 QSAKLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAP 237
               | :||||| ::|:|||:|||||   ||||||| :|| || |||||:||||||||:|||
Db        181 QQANVADPGAT-NRAAPVISVIIPESETYNNTLDHSVCTNFEASELGDEVEANFTALFAP 239

Qy        238 PIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQ 297
               ||||:| ||||| |||:|||:||||| |||||||||:||::||||| :||!:|| :|||||
Db        240 AIRARIEKHLPGVQLTDDDVVSLMDMCSFDTVARTADASELSPFCAIFTHNEWKKYDYLQ 299

Qy        298 SLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYA 357
```

```
              ||||||||||||||||:|||:|| ||||||||:|||||||||| ||||:||||||||||:|
Db        300 SLGKYYGYGAGNPLGPAQGIGFTNELIARLTNSPVQDHTSTNSTLDSDPATFPLNATIYV 359

Qy        358 DFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAE 417
              |||||| |: |||:||||||:||| || ||  :|::|:||| ||| |||| | |||::|
Db        360 DFSHDNGMIPIFFAMGLYNGTEPLSQTSEESTKESNGYSASWAVPFGARAYFETMQCKSE 419

Qy        418 KEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              |||||| |:||||||||||| ||||||||  |||:|||:||||||  |: |:
Db        420 KEPLVRALINDRVVPLHGCAVDKLGRCKLKDFVKGLSWARSGGNSEQSFS 469
```

RESULT 12
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
;   APPLICANT: Robert F.M. Van Gorcom
;   APPLICANT: Willem Van Hartingsveldt
;   APPLICANT: Petrus A. Van Paridon
;   APPLICANT: Annemarie E. Veenstra
;   APPLICANT: Rudolf G.M. Luttin
;   APPLICANT: Gerardus Selten
;   TITLE OF INVENTION: Cloning and Expression of Microbial
;   TITLE OF INVENTION: Phytase
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Morrison & Foerster
;   STREET: 545 Middlefield Road, Suite 200
;   CITY: Menlo Park
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94025-3471
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   SOFTWARE:
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/079,709
;   FILING DATE: 02-FEB-2002
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/233,510
;   FILING DATE: 20-JAN-1999
;   APPLICATION NUMBER: 07/688,578
;   FILING DATE: 24-MAY-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Murashige, Kate H.
;   REGISTRATION NUMBER: 29,959
;   REFERENCE/DOCKET NUMBER: 24615-20026.00
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-327-7250
;   TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 467 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-10-079-709-32

```
  Query Match             75.4%;  Score 1862;  DB 15;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 1.7e-179;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              |||  |||  :  | | ||| |:     |  ||||||| |||||  | |||||||:||||||:|
Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
               | |||:|| |||||| |||||||||||| || |||||||| ||:||| | ||||||||||
```

```
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180

Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240

Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300

Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420

Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467

Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 13
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-229-358-5

  Query Match           75.4%;  Score 1862;  DB 15;  Length 467;
  Best Local Similarity   74.5%;  Pred. No. 1.7e-179;
  Matches  348;  Conservative   44;  Mismatches   75;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGIALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60

Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120

Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180

Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240

Db        181 KLKDPRAQPGQSSPKIDVVISEASSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300

Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420

Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467

Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA 467


RESULT 14
US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
;  APPLICANT: KONDO, HIDEMASA
;  APPLICANT:  ANAZAWA, HIDEHARU
;  APPLICANT:  KANEKO, SYUNICHI
;  APPLICANT:  NAGASHIMA, TADASHI
;  APPLICANT:  TANGE, TATSUYA
;  TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
;  FILE REFERENCE: 081356/0166
;  CURRENT APPLICATION NUMBER: US/09/929,060
;  CURRENT FILING DATE:  2001-08-15
;  PRIOR APPLICATION NUMBER: 09/543,744
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: 09/155,855
;  PRIOR FILING DATE: 1998-10-05
;  PRIOR APPLICATION NUMBER: JP 084314/1996
;  PRIOR FILING DATE: 1996-04-05
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-09-929-060-3

  Query Match           75.1%;  Score 1855;  DB 9;  Length 467;
  Best Local Similarity   73.4%;  Pred. No. 8.7e-179;
  Matches  343;  Conservative   51;  Mismatches   73;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGIALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60

Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSTCDTVDQGYQCFSETSHLWGQYAPFFSLANK 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120

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Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180

Db        121 YSLGADDLTPFGEQELVNSGVKFYQRYESLTRNIVPFIRSSGSSRVIASGNKFIEGFQST 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240

Db        181 KLKDPRAQPGQSSPKIDVVISEASTSNNTLDPGTCTVFEDSELADDIEANFTATFVPSIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300

Db        241 QRLENDLSGVSLTDTEVTYLMDMCSFDTISTSTVDIKLSPFCDLFTHEEWINYDYLQSLN 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420

Db        361 HDNGIISILFALGLYNGTKPLSSTTAENITQTDGFSSAWTVPFASRMYVEMMQCQSEQEP 420
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Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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Db        421 LVRVLVNDRVVPLHGCPVDALGRCTRDSFVKGLSFARSGGDWGECFA 467


RESULT 15
US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
;  APPLICANT: Svendsen, Allan
;  TITLE OF INVENTION: Phytase Variants
;  FILE REFERENCE: 5618.500-US
;  CURRENT APPLICATION NUMBER: US/10/083,452
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: US/09/273,871
;  PRIOR FILING DATE: 1999-03-22
;  PRIOR APPLICATION NUMBER: PA 1998 00407
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: PA 1998 00806
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: PA 1998 01176
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: PA 1999 00091
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/080,129
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/090,675
;  PRIOR FILING DATE: 1998-06-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus ficuum
US-10-083-452-11

  Query Match             74.9%;  Score 1850;  DB 14;  Length 467;
  Best Local Similarity   74.1%;  Pred. No. 2.8e-178;
  Matches  346;  Conservative   44;  Mismatches   77;  Indels    0;  Gaps    0;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
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Db          1 MGVSAVLLPLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
              | |||:|| ||:||| |:|||||:|||| || ||||:|||| ||:||' | ||:|||||||
Db         61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |:|||||||||||::|||||||||:||::| | ||||:|:||| ||||| :|||:||||
Db        121 YSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQST 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              || || | | |:|| |:|:| | :  ||||| | || ||:||| | |||||||  | | ||
Db        181 KLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDAIQLSPFCDLFTHDEWIQYDYLQSLG 300
               |||  | || ||| :;  |||| ||||:: ::  |:|||||||||||||| |||||||
Db        241 QRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLK 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSINHTLDSNPATFPLNATLYADFS 360
              ||||:|||||||| |||| |||||||||||| | ||:|||||:|||||| :|||||||
Db        301 KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLKSTLYADFS 360

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              ||| ::|| ||||||||||||||||:||:| :|||::::|||||:| |||||||:||: |
Db        361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQAP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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Search completed: October  3, 2003, 08:12:28
Job time : 108.714 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.9581 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-26
Perfect score: 2470
Sequence: 1 MGVFVVLLSIATLFGSTSGT.....DFVEGLSFARSGGNWEECFA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2311	93.6	467	4	US-09-273-871A-9	Sequence 9, Appli
2	2185	88.5	441	3	US-09-121-425-1	Sequence 1, Appli
3	2185	88.5	441	4	US-09-634-493A-1	Sequence 1, Appli
4	2173	88.0	467	3	US-09-121-425-2	Sequence 2, Appli
5	2173	88.0	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1902	77.0	465	3	US-08-868-435-33	Sequence 33, Appl
7	1902	77.0	465	4	US-08-744-231-33	Sequence 33, Appl
8	1902	77.0	465	4	US-09-044-718-78	Sequence 78, Appl
9	1902	77.0	465	4	US-09-636-499-6	Sequence 6, Appli
10	1902	77.0	465	4	US-09-273-871A-8	Sequence 8, Appli
11	1894	76.7	465	4	US-09-044-718-80	Sequence 80, Appl
12	1893	76.6	465	4	US-09-044-718-79	Sequence 79, Appl
13	1892.5	76.6	439	4	US-09-044-718-3	Sequence 3, Appli
14	1892.5	76.6	449	4	US-09-044-718-12	Sequence 12, Appl
15	1890	76.5	465	4	US-09-044-718-81	Sequence 81, Appl
16	1868	75.6	469	4	US-09-044-718-82	Sequence 82, Appl
17	1866	75.5	467	1	US-07-923-724-8	Sequence 8, Appli
18	1866	75.5	467	2	US-08-609-426A-8	Sequence 8, Appli
19	1866	75.5	467	2	US-08-374-652C-2	Sequence 2, Appli
20	1862	75.4	467	1	US-08-151-574-32	Sequence 32, Appl
21	1862	75.4	467	1	US-08-146-424-20	Sequence 20, Appl
22	1862	75.4	467	1	US-08-693-709-2	Sequence 2, Appli
23	1862	75.4	467	2	US-08-419-448-32	Sequence 32, Appl
24	1862	75.4	467	2	US-08-819-825-3	Sequence 3, Appli
25	1862	75.4	467	3	US-09-163-642-3	Sequence 3, Appli
26	1862	75.4	467	4	US-09-233-510-32	Sequence 32, Appl
27	1862	75.4	467	4	US-09-636-499-5	Sequence 5, Appli
28	1855	75.1	467	3	US-09-155-855-3	Sequence 3, Appli
29	1855	75.1	467	4	US-09-543-744-3	Sequence 3, Appli
30	1855	75.1	467	4	US-09-929-060-3	Sequence 3, Appli
31	1850	74.9	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1843	74.6	462	4	US-09-636-499-12	Sequence 12, Appl
33	1841	74.5	466	3	US-08-868-435-12	Sequence 12, Appl
34	1841	74.5	466	4	US-08-744-231-12	Sequence 12, Appl
35	1826	73.9	466	3	US-08-868-435-35	Sequence 35, Appl
36	1826	73.9	466	4	US-08-744-231-35	Sequence 35, Appl
37	1820	73.7	444	4	US-09-044-718-1	Sequence 1, Appli
38	1813.5	73.4	463	3	US-08-868-435-29	Sequence 29, Appl
39	1813.5	73.4	463	4	US-08-744-231-29	Sequence 29, Appl
40	1813.5	73.4	463	4	US-09-273-871A-10	Sequence 10, Appl
41	1813	73.4	443	3	US-09-155-855-1	Sequence 1, Appli
42	1813	73.4	443	4	US-09-543-744-1	Sequence 1, Appli
43	1813	73.4	443	4	US-09-929-060-1	Sequence 1, Appli
44	1808	73.2	443	3	US-09-155-855-2	Sequence 2, Appli
45	1808	73.2	443	4	US-09-543-744-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Query Match 93.6%; Score 2311; DB 4; Length 467;
Best Local Similarity 93.1%; Pred. No. 3.9e-235;
Matches 435; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

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Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
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Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
              ||||||||  ||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYN 120

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||| ||||||||||||||||||||:|||||||||||||||||||||||||||
Db        121 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 180

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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Db        181 KLADPGSQPHQASPVIDVIIPEGSGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              ||||| |||| |||||||| |||||||:||||||||:|||| ||||||| ||||||||||
Db        241 ARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSPFCALFTHDEWRQYDYLQSLG 300

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Db        301 KYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSINHTLDSNPATFPLNATLYADFS 360

Qy        361 HDNIMVSIFFALGLYNGIKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              ||:|:|||||||||||| ||||||||||||||||:|||||| |||||||||||:|||||
Db        361 HDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWTVPFGARAYVEMMQCQAEKEP 420

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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Db        421 LVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGGNWAECFA 467


RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

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  Best Local Similarity   92.7%;  Pred. No. 7.1e-222;
  Matches  409;  Conservative   13;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         27 NSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 86
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Db          1 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 60

Qy         87 PTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
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Db         61 PTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

Qy        147 YKALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY 206
              ||||||||||:|||||||||||||||||||||||||||: |||||||:|||||||:||
Db        121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy        207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
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Db        181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

Qy        267 DTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
              :|||||||||:||||| |||||||||||||||||||||||||||||||||||| ||||||
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Qy        327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
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Db        301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy        387 ESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
              |||||||||:||||||| |||||||||:|||||||||||||||||||| ||||||||||
Db        361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy        447 DDFVEGLSFARSGGNWEECFA 467
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Db        421 DDFVEGLSFARSGGNWAECFA 441


RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-1

  Query Match             88.5%;  Score 2185;  DB 4;  Length 441;
  Best Local Similarity   92.7%;  Pred. No. 7.1e-222;
  Matches  409;  Conservative   13;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         27 NSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARY 86
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Db          1 NSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDESAISPDVPDDCRVTFVQVLSRHGARY 60

Qy         87 PTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRR 146
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Db         61 PTSSKSKAYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGENQMVNSGIKFYRR 120

Qy        147 YKALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGY 206
              ||||||||||:|||||||||||||||||||||||||||: |||||||:|||||||:||
Db        121 YKALARKIVPFIRASGSDRVIASAEKFIEGFQSAKLADPGSQPHQASPVIDVIIPEGSGY 180

Qy        207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPF 266
              ||||||| |||||:|||||||||||||:||| ||||||| |||| ||||||| ||||||
Db        181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPF 240

Qy        267 DTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIAR 326
              :|||||||||:||||| |||||||||||||||||||||||||||||||||||| ||||||
Db        241 ETVARTSDATELSPFCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIAR 300

Qy        327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSV 386
              || ||||||||||||||||||||||||||||||:|:|||||||||| ||||||||||||
Db        301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSV 360

Qy        387 ESIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKR 446
              |||||||||:||||||| |||||||||:|||||||||||||||||||| ||||||||||
Db        361 ESIEETDGYSASWTVPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKR 420

Qy        447 DDFVEGLSFARSGGNWEECFA 467
              ||||||||||||||| ||||
Db        421 DDFVEGLSFARSGGNWAECFA 441


RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
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;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 467
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:consensus
;    OTHER INFORMATION: sequence
US-09-121-425-2

  Query Match             88.0%;  Score 2173;  DB 3;  Length 467;
  Best Local Similarity   85.2%;  Pred. No. 1.4e-220;
  Matches  415;  Conservative   13;  Mismatches   19;  Indels   40;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||:||  ||
Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
              ||||||||  |||||||||||||||,|||||||| |||                    |||
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSA--------------------TYN 100

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              ||||||||||||| ||||||||||||||||||||||:||||'|||||||||||||:|||
Db        101 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160

Qy        181 KLADPGANPHQASPVIN--------------------VIIPEGAGYNNTLDHGLCTAFEE 220
              ||||||: ||||||||:                    ||||||:|||||||| ||||||:
Db        161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy        221 SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSP 280
              ||||||||||||||:||| |||||||  |||| |||||||  ||||||:||||||||:|||
Db        221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

Qy        281 FCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNH 340
              || ||||||| |||||||||||||||||||||||||||| ||||||| |||||||||||
Db        281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy        341 TLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWT 400
              |||||||||||||||||||||||:|:|||||,||||||, ||||||||||||||:|||'
Db        341 TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

Qy        401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGG 460
              ||| ||||||||||:|||||||||||||||||| |||,||||||||||||||,|||
Db        401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460

Qy        461 NWEECFA 467
              || ||||
Db        461 NWAECFA 467


RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 467
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:consensus
;    OTHER INFORMATION: sequence
US-09-634-493A-2

  Query Match             88.0%;  Score 2173;  DB 4;  Length 467;
  Best Local Similarity   85.2%;  Pred. No. 1.4e-220;
  Matches  415;  Conservative   13;  Mismatches   19;  Indels   40;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||:||  ||
Db          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPYFSLEDE 60

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
              ||||||||  |||||||||||||||||||||||||| |||                    |||
Db         61 SAISPDVPDDCRVTFVQVLSRHGARYPTSSKSKAYSA--------------------TYN 100

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||,|||||  ||||||||:||||||||||||||:||||||||||||||,||||||
Db        101 YTLGADDLTPFGENQMVNSGIKFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGFQSA 160

Qy        181 KLADPGANPHQASPVIN--------------------VIIPEGAGYNNTLDHGLCTAFEE 220
              |||||||: ||||||||:                    ||||||:|||||||| ||||||:
Db        161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGKYAFLKVIIPEGSGYNNTLDHGTCTAFED 220

Qy        221 SELGDDVEANFTAVFAPPIRARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSP 280
              ||||||||||||||:||| |||||||  |||| |||||||  ||||||:||||||||:|||
Db        221 SELGDDVEANFTALFAPAIRARLEADLPGVTLTDEDVVYLMDMCPFETVARTSDATELSP 280

Qy        281 FCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNH 340
              || ||||||| |||||||||||||||||||||||||||| ||||||| |||||||||||
Db        281 FCALFTHDEWRQYDYLQSLGKYYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340

Qy        341 TLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWT 400
              |||||||||||||||||||||||:|:|||||||||||| ||||||||||||:||||||||
Db        341 TLDSNPATFPLNATLYADFSHDNSMISIFFALGLYNGTAPLSTTSVESIEETDGYSASWT 400

Qy        401 VPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGG 460
              ||| ||||||||||:|||||||||||||||||| |||||||||||||||||||||||||
Db        401 VPFGARAYVEMMQCQAEKEPLVRVLVNDRVVPLHGCAVDKLGRCKRDDFVEGLSFARSGG 460

Qy        461 NWEECFA 467
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Db        461 NWAECFA 467


RESULT 6
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-868-435-33

  Query Match             77.0%;  Score 1902;  DB 3;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 5.9e-192;
  Matches  360;  Conservative   37;  Mismatches   68;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              |     ||| | |        |    | | |||||| |||| |  ||||||||||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPAISHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
               ::|  :|| ||:| |||||||||||||||||  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:||||||||:|||||||  :|||:|||||||||||  |||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :|||||||:|| || |:|||:| |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:||||| ||||||||||:|||||| ||||:|| :|:||||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||:|| |||||||| |||||||||| || ||||||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||||:|||  |||||  :| |||:||| |||  |||| | |||::||||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:||||||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 7
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
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;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33

  Query Match             77.0%;  Score 1902;  DB 4;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 5.9e-192;
  Matches  360;  Conservative   37;  Mismatches   68;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              |     ||| | |     |   | | |||||| |||| ;  |||:|||||||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                ::|  :|| ||:| ||||||||||||||||||||  |: ||| .|| ||:|:|:|||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:| ||||||:|||||| :|||:|||||||||| ||||||| :
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              ||||||  ::|:| |:|||||   :||||||||:|| || |:|||:, |||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | |||:| ||||||:|||| ||||||||||:|||| |||||:|| :|:|:|||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:|| |||||||| |||||||||| || ||||||||.|:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| |||:| :| |||:||| ||| |||| | :|||:|||||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
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Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 8
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 78
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-78

  Query Match             77.0%;  Score 1902;  DB 4;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 5.9e-192;
  Matches  360;  Conservative   37;  Mismatches   68;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
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Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                ::|  :|| ||:| ||||||||||||||||||||  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:|||||||:|||||| :|||:|||||||||| ||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :||||||||:|| || |:|||:| ||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESEIFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | |||:| ||||||:|||| ||||||||||:|||| |||||:|| :|:|:|||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
              ||||||||||||||||:|| |||||||| |||||||||| || ||||||||.|:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||:||| |||:| :| |||:||| ||| |||| | :|||:|||||
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||:|| :|||||:| :|||:|||:|||||| :||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 9
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
;  APPLICANT:  Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION:  Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Sam
;  FILE REFERENCE:  GC586-2
;  CURRENT APPLICATION NUMBER: US/09/636,499
;  CURRENT FILING DATE:  2000-08-11
;  PRIOR APPLICATION NUMBER:  US 60/148,960
;  PRIOR FILING DATE:  1999-08-13
;  NUMBER OF SEQ ID NOS:  34
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-636-499-6

  Query Match             77.0%;  Score 1902;  DB 4;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 5.9e-192;
  Matches  360;  Conservative   37;  Mismatches   68;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              |     ||| | |       |   | | |||||| |||| |  |||||||||||| ||
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
                ::|  :|| ||:| ||||||||||||||||||||  |: ||| ||| ||||:|||||||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:|||||||:|||||| :|||:|||||||||| ||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :||||||||:|| || |:|||:| ||||:||| ||
Db        180 KLADPGAT-NRAAPAISVIIPESEIFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238
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Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 10
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
;  APPLICANT:  Svendsen, Allan
;  TITLE OF INVENTION:  Phytase Variants
;  FILE REFERENCE:  5618.500-US
;  CURRENT APPLICATION NUMBER: US/09/273,871A
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER:  PA 1998 00407
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  PA 1998 00806
;  PRIOR FILING DATE:  1998-06-19
;  PRIOR APPLICATION NUMBER:  PA 1998 01176
;  PRIOR FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  PA 1999 00091
;  PRIOR FILING DATE:  1999-01-22
;  PRIOR APPLICATION NUMBER:  60/080,129
;  PRIOR FILING DATE:  1998-03-31
;  PRIOR APPLICATION NUMBER:  60/090,675
;  PRIOR FILING DATE:  1998-06-25
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-273-871A-8

  Query Match             77.0%;  Score 1902;  DB 4;  Length 465;
  Best Local Similarity   77.1%;  Pred. No. 5.9e-192;
  Matches  360;  Conservative   37;  Mismatches   68;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
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Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGIKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 11
US-09-044-718-80
; Sequence 80, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-80

  Query Match             76.7%;  Score 1894;  DB 4;  Length 465;
  Best Local Similarity   76.9%;  Pred. No. 4.1e-191;
  Matches  359;  Conservative   37;  Mismatches   69;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCIAFEESELGDDVEANFTAVFAPPIR 240
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKES 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465
```

```
RESULT 12
US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-79

  Query Match             76.6%;  Score 1893;  DB 4;  Length 465;
  Best Local Similarity   76.9%;  Pred. No. 5.3e-191;
  Matches  359;  Conservative   37;  Mismatches   69;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
              |     ||| | |       |    | | |||||| |||| |  ||||||||||||| :|
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNATAFKGKYAFLKTYN 120
               ::|  :|| ||:| ||||||||||||||||||||  |: ||| ||| |||:|||:|||
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
              |||||||||||||||:||||||||:|||||| :|||:|||||||||| |||||||| |
Db        120 YTLGADDLTPFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
              |||||||  ::|:| |:|||||   :|||||||:|| || |:|||:| |||||:||| :|
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLTDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
              || | ||||| |||||||:|||| |||||||||||:|||||| ||||:|| :|:|||||
Db        239 ARAEKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHISTNHTLDSNPATFPLNATLYADFS 360
              |||||||||||||||||:| |||:|||| ||||||||||:|| || |||| |||||||:| |||
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHISTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNIMVSIFFALGLYNGTKPLSITTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
              |||:|||||||||||||||: |' ||||| :| |||:||| ||| |||| | |:|:: |||
Db        359 HDNSMVSIFFALGLYNGTEGLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
              ||| |:|||||||||| |||||||| :|||:|||:|||:||| |||:
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


RESULT 13
US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-3

  Query Match             76.6%;  Score 1892.5;  DB 4;  Length 439;
  Best Local Similarity   80.0%;  Pred. No. 5.4e-191;
  Matches  352;  Conservative   37;  Mismatches   50;  Indels    2;  Gaps    1;

Qy         28 SHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 87
              | |||||| |||| |  |||||||||||| || ::|  :|| ||:| ||||||||||
Db          1 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 60

Qy         88 TSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRY 147
              ||||||||  |: ||| ||| |||||:|||||||||||||||||||||||:||||||:||
Db         61 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 120

Qy        148 KALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYN 207
              ||||| :|||:|||||||||||| |||||||| |||||||  ::|:| |:|||||   :|
Db        121 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGAT-NRAAPAISVIIPESETFN 179

Qy        208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLIDEDVVNLMDMCPFD 267
              |||||:|| || |:|||:| |||||:||| |||| | ||||| ||||||:|||| ||
Db        180 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLIDEDVVSLMDMCSFD 239

Qy        268 TVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
              ||||||||:|||||| ||||:|| :|:|||||||||||||||||||||:|| |||||||
Db        240 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 299

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSITTSVE 387
              | |||||||||| || ||||||||||:| |||||:|||||||||||||||:|||  ||||
Db        300 TRSPVQDHTSTNSTLVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 359

Qy        388 SIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
              | :| |||:||| |||| | |||::||||||| |:|||||||||| |'||||||  :
Db        360 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 419

Qy        448 DFVEGLSFARSGGNWEECFA 467
              |||:|||:|||||| |||:
Db        420 DFVKGLSWARSGGNWGECFS 439


RESULT 14
US-09-044-718-12
; Sequence 12, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
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;   ORGANISM: Aspergillus fumigatus
US-09-044-718-12

  Query Match             76.6%;  Score 1892.5;  DB 4;  Length 449;
  Best Local Similarity   80.0%;  Pred. No. 5.6e-191;
  Matches  352;  Conservative   37;  Mismatches   50;  Indels    1;  Gaps    1;

Qy         28 SHSCDTVDGGYQCFPEISHLWGQYSPFFSLADESAISPDVPKGCRVTFVQVLSRHGARYP 87
Db         11 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 70

Qy         88 TSSKSKKYSALIEAIQKNATAFKGKYAFLKTYNYTLGADDLTPFGEQQMVNSGIKFYRRY 147
Db         71 TSSKSKKYKKLVTAIQANATDFKGKFAFLKTYNYTLGADDLTPFGEQQLVNSGIKFYQRY 130

Qy        148 KALARKIVPFVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVINVIIPEGAGYN 207
Db        131 KALARSVVPFIRASGSDRVIASGEKFIEGFQQAKLADPGAT-NRAAPAISVIIPESETFN 189

Qy        208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARLEAHLPGVNLIDEDVVNLMDMCPFD 267
Db        190 NTLDHGVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVVSLMDMCSFD 249

Qy        268 TVARTSDATQLSPFCDLFTHDEWIQYDYLQSLGKYYGYGAGNPLGPAQGVGFVNELIARL 327
Db        250 TVARTSDASQLSPFCQLFTHNEWKKYNYLQSLGKYYGYGAGNPLGPAQGIGFTNELIARL 309

Qy        328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGIKPLSTTSVE 387
Db        310 TRSPVQDHTSTNSILVSNPATFPLNATMYVDFSHDNSMVSIFFALGLYNGTEPLSRTSVE 369

Qy        388 SIEETDGYAASWTVPFAARAYVEMMQCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCKRD 447
Db        370 SAKELDGYSASWVVPFGARAYFETMQCKSEKEPLVRALINDRVVPLHGCDVDKLGRCKLN 429

Qy        448 DFVEGLSFARSGGNWEECFA 467
Db        430 DFVKGLSWARSGGNWGECFS 449


RESULT 15
US-09-044-718-81
; Sequence 81, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-81

  Query Match             76.5%;  Score 1890;  DB 4;  Length 465;
  Best Local Similarity   76.7%;  Pred. No. 1.1e-190;
  Matches  358;  Conservative   38;  Mismatches   69;  Indels    2;  Gaps    2;

Qy          1 MGVFVVLLSIATLFGSTSGTALGPRGNSHSCDTVDGGYQCFPEISHLWGQYSPFFSLADE 60
Db          1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLEDE 59

Qy         61 SAISPDVPKGCRVTFVQVLSRHGARYPTSSKSKKYSALIEAIQKNAIAFKGKYAFLKIYN 120
Db         60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYKKLVTAIQANATDFKGKFAFLKTYN 119

Qy        121 YTLGADDLTPFGEQQMVNSGIKFYRRYKALARKIVPFVRASGSDRVIASAEKFIEGFQSA 180
Db        120 YTLGADDLTAFGEQQLVNSGIKFYQRYKALARSVVPFIRASGSDRVIASGEKFIEGFQQA 179

Qy        181 KLADPGANPHQASPVINVIIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db        180 KLADPGAT-NRAAPAISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

Qy        241 ARLEAHLPGVNLIDEDVVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIQYDYLQSLG 300
Db        239 ARAKKHLPGVTLTDEDVVSLMDMCSFDTVARTSDASQLSPFCQLFTHNEWKKYNYLQSLG 298

Qy        301 KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db        299 KYYGYGAGNPLGPAQGIGFTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYVDFS 358

Qy        361 HDNTMVSIFFALGLYNGIKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMQCEAEKEP 420
Db        359 HDNSMVSIFFALGLYNGTEPLSRTSVESAKELDGYSASWVVPFGARAYFETMQCKSEKEP 418

Qy        421 LVRVLVNDRVVPLHGCGVDKLGRCKRDDFVEGLSFARSGGNWEECFA 467
Db        419 LVRALINDRVVPLHGCDVDKLGRCKLNDFVKGLSWARSGGNWGECFS 465


Search completed: October  3, 2003, 07:47:46
Job time : 14.9581 secs
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GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 07:48:21 ; Search time 21.3866 Seconds
(without alignments)
5642.336 Million cell updates/sec

Title: US-09-488-265B-25
Perfect score: 2525
Sequence: 1 tatatgaattcatgggcgtg.....ttcgcttaagaattcatata 1426

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310856 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=oct3.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265_@CGN_1_1_99_@runat_03102003_074813_12239 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2311	91.5	467	4	US-09-273-871A-9	Sequence 9, Appli
2	2185	86.5	441	3	US-09-121-425-1	Sequence 1, Appli
3	2185	86.5	441	4	US-09-634-493A-1	Sequence 1, Appli
4	2173	86.1	467	3	US-09-121-425-2	Sequence 2, Appli
5	2173	86.1	467	4	US-09-634-493A-2	Sequence 2, Appli
6	1902	75.3	465	3	US-08-868-435-33	Sequence 33, Appl
7	1902	75.3	465	4	US-08-744-231-33	Sequence 33, Appl
8	1902	75.3	465	4	US-09-044-718-78	Sequence 78, Appl
9	1902	75.3	465	4	US-09-636-499-6	Sequence 6, Appli
10	1902	75.3	465	4	US-09-273-871A-8	Sequence 8, Appli
11	1894	75.0	465	4	US-09-044-718-80	Sequence 80, Appl
12	1893	75.0	465	4	US-09-044-718-79	Sequence 79, Appl
13	1892.5	75.0	439	4	US-09-044-718-3	Sequence 3, Appli
14	1892.5	75.0	449	4	US-09-044-718-12	Sequence 12, Appl
15	1890	74.9	465	4	US-09-044-718-81	Sequence 81, Appl
16	1868	74.0	469	4	US-09-044-718-82	Sequence 82, Appl
17	1866	73.9	467	1	US-07-923-724-8	Sequence 8, Appli
18	1866	73.9	467	2	US-08-609-426A-8	Sequence 8, Appli
19	1866	73.9	467	2	US-08-374-652C-2	Sequence 2, Appli
20	1862	73.7	467	1	US-08-151-574-32	Sequence 32, Appl
21	1862	73.7	467	1	US-08-146-424-20	Sequence 20, Appl
22	1862	73.7	467	1	US-08-693-709-2	Sequence 2, Appli
23	1862	73.7	467	2	US-08-419-448-32	Sequence 32, Appl
24	1862	73.7	467	2	US-08-819-825-3	Sequence 3, Appli
25	1862	73.7	467	3	US-09-163-642-3	Sequence 3, Appli
26	1862	73.7	467	4	US-09-233-510-32	Sequence 32, Appl
27	1862	73.7	467	4	US-09-636-499-5	Sequence 5, Appli
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31	1850	73.3	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1843	73.0	462	4	US-09-636-499-12	Sequence 12, Appl
33	1841	72.9	466	3	US-08-868-435-12	Sequence 12, Appl
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35	1826	72.3	466	3	US-08-868-435-35	Sequence 35, Appl
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37	1820	72.1	444	4	US-09-044-718-1	Sequence 1, Appli
38	1813.5	71.8	463	3	US-08-868-435-29	Sequence 29, Appl
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41	1813	71.8	443	3	US-09-155-855-1	Sequence 1, Appli
42	1813	71.8	443	4	US-09-543-744-1	Sequence 1, Appli
43	1813	71.8	443	4	US-09-929-060-1	Sequence 1, Appli
44	1808	71.6	443	3	US-09-155-855-2	Sequence 2, Appli
45	1808	71.6	443	4	US-09-543-744-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Alignment Scores:
Pred. No.: 6.13e-212 Length: 467
Score: 2311.00 Matches: 435
Percent Similarity: 95.93% Conservative: 13

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Query Match:            91.52%        Indels:        0
DB:                     4             Gaps:          0

US-09-488-265B-25 (1-1426) x US-09-273-871A-9 (1-467)

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Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
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Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
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Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              |||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
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Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
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Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
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Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
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              ||||||||||||||||||||||||||||||||||||||||||||:::|||:||||:|||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||   ||||||||||||||||||||||||||||||:::|||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              ||||||||||||||||||||||||||||||||||||||||||:|||||   |||||||||
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Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
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Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
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RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-1

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Query Match:            86.53%          Indels:         0
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Qy        150 TTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGAC 209
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Db         21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40

Qy        210 GTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATAC 269
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Qy        270 CCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCT 329
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Qy        330 ACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 389
Db         81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

Qy        390 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGA 449
Db        101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120

Qy        450 TACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTT 509
Db        121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140

Qy        510 ATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGT 569
Db        141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160

Qy        570 GCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTAC 629
Db        161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180

Qy        630 AACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGAC 689
Db        181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

Qy        690 GTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCAC 749
Db        201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220

Qy        750 TTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTC 809
Db        221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240

Qy        810 GACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACT 869
Db        241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260

Qy        870 CACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGT 929
Db        261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280

Qy        930 GCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGA 989
Db        281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

Qy        990 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCA 1049
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Qy       1050 GCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTT 1109
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Qy       1110 TCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTT 1169
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Qy       1170 GAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACTGTTCCATTCGCTGCTAGA 1229
Db        361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380

Qy       1230 GCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1289
Db        381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

Qy       1290 AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGA 1349
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Qy       1350 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTC 1409
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Qy       1410 GCT 1412
Db        441 Ala 441
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RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/634,493A
;  CURRENT FILING DATE:  2000-08-08
;  PRIOR APPLICATION NUMBER: US/09/121,425
;  PRIOR FILING DATE: 1998-07-23
;  PRIOR APPLICATION NUMBER: EPO 97112688.3
;  PRIOR FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 441
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-634-493A-1

Alignment Scores:
Pred. No.:                6.27e-200       Length:          441
Score:                    2185.00         Matches:         409
Percent Similarity:       95.69%          Conservative:    13
Best Local Similarity:    92.74%          Mismatches:      19
Query Match:              86.53%          Indels:          0
DB:                       4               Gaps:            0

US-09-488-265B-25 (1-1426) x US-09-634-493A-1 (1-441)

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Qy        150 TTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGAC 209
Db         21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40

Qy        210 GTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATAC 269
Db         41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60

Qy        270 CCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCT 329
Db         61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80

Qy        330 ACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGAC 389
Db         81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100

Qy        390 GACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGA 449
Db        101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120

Qy        450 TACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTT 509
Db        121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140

Qy        510 ATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGT 569
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Db        141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160

Qy        570 GCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTAC 629
              :::   ||||||||||||||||||||||||||:::|||||||||||||||||||:::|||||
Db        161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180

Qy        630 AACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGAC 689
              ||||||||||||||||||||    ||||||||||||||||:::||||||||||||||||
Db        181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200

Qy        690 GTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCAC 749
              ||||||||||||||||||||:::||||||||||    ||||||||||||||||||||||
Db        201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220

Qy        750 TTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTC 809
              ||||||||||||    ||||||||||||||||||||    ||||||||||||||||||||
Db        221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240

Qy        810 GACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACT 869
              :::||||||||||||||||||||||||||||:::||||||||||||||||    ||||||||||
Db        241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260

Qy        870 CACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGT 929
              ||||||||||||    ||||||||||||||||||||||||||||||||||||||||||||
Db        261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280

Qy        930 GCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGA 989
              ||||||||:||||||||||||||:||||||||||||||||    ||||||||||||||||||
Db        281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300

Qy        990 TTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCA 1049
              ||||||    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320

Qy       1050 GCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTT 1109
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||:::
Db        321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340

Qy       1110 TCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTT 1169
              ||||||||||||||||||||||||||||||||    ||||||||||||||||||||||
Db        341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360

Qy       1170 GAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACTGTTCCATTCGCTGCTAGA 1229
              ||||||||||||||||||||||:|||||:::||||||||||||||||,||||||    |||||
Db        361 GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380

Qy       1230 GCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTT 1289
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400

Qy       1290 AACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGA 1349
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420

Qy       1350 GACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTC 1409
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db        421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440

Qy       1410 GCT 1412
              |||
Db        441 Ala 441

RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
;  APPLICANT: Lehmann, Martin
;  TITLE OF INVENTION: Consensus Phytases
;  FILE REFERENCE: consensus phytases 13239
;  CURRENT APPLICATION NUMBER: US/09/121,425
;  CURRENT FILING DATE: 1998-07-23
;  EARLIER APPLICATION NUMBER: EPO 97112688.3
;  EARLIER FILING DATE: 1997-07-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:consensus
;   OTHER INFORMATION: sequence
US-09-121-425-2

Alignment Scores:
Pred. No.:                9.07e-199       Length:          467
Score:                    2173.00         Matches:         415
Percent Similarity:       87.89%          Conservative:    13
Best Local Similarity:    85.22%          Mismatches:      19
Query Match:              86.06%          Indels:          40
DB:                       3               Gaps:            2

US-09-488-265B-25 (1-1426) x US-09-121-425-2 (1-467)

Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||    ||||||
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
              ||||||||||||||||||||||||      ||||||||||||||||||||||||||||||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        252 AGACACGGTGCTAGATACCCAACTTCITCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla--------- 97

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
                                                                  ||||||||||
Db         98 ----------------------------------------------------ThrTyrAsn 100

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC--------- 602
              ||||||||||||||||:::    ||||||||||||||||||||||:::
Db        161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

Qy        603 ----------------------------------------------------GTTATTATI 611
                                                                  |||||||||
Db        181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
              |||||||||:::||||||||||||||||||||||||||||    ||||||||||||||:::
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
              ||||||||||||||||||||||||||||||||||||||||||:::||||||||    ||||||
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
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Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
Db        461 AsnTrpAlaGluCysPheAla 467
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RESULT 5
US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-2

Alignment Scores:

Pred. No.:	9.07e-199	Length:	467
Score:	2173.00	Matches:	415
Percent Similarity:	87.89%	Conservative:	13
Best Local Similarity:	85.22%	Mismatches:	19
Query Match:	86.06%	Indels:	40
DB:	4	Gaps:	2

US-09-488-265B-25 (1-1426) x US-09-634-493A-2 (1-467)

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Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla--------- 97

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
Db         98 ----------------------------------------------------ThrTyrAsn 100

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
Db        101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
Db        121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
Db        141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC--------- 602
Db        161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180

Qy        603 ----------------------------------------------------GTTATTATT 611
Db        181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
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Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
              ||||||||||:::|||:::||||||||||||||||||||||||||||||||||||||||||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              ||||||||||||||||||||||||||||||||||||||||||||:::||||||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||   ||||||||||||||||||||||||||||||:::|||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
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Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 6
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/868,435
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/744,231
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
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US-08-868-435-33

Alignment Scores:
Pred. No.:                6.6e-173        Length:          465
Score:                    1902.00         Matches:         360
Percent Similarity:       85.01%          Conservative:    37
Best Local Similarity:    77.09%          Mismatches:      68
Query Match:              75.33%          Indels:          2
DB:                       3               Gaps:            2

US-09-488-265B-25 (1-1426) x US-08-868-435-33 (1-465)

Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
              |||                 |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              |||           |||   |||   ||||||||||||||||||   ||||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
              |||       |||||||||||||||||||||||||||||||||||||||||   ||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGln 59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
              ::::::|||       :::||||||   ||||||:::|||   ||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              ||||||||||||||||||||||||||||||||||||||||||||||||      ||||:::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
              |||||||||   |||||||||   ||||||||||||:::||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
              ||||||||||||||||||||||||||||||:|||||||||||||:::||||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
              ||||||||||||:::||||||||||||||||||||   :::|||||||||:::||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
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Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
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Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
              ||||||||||||||||||||||      ::::::|||:::|||   |||:::||||||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
              ||||||      :::|||||||||||||||||||||||:::|||||||   |||:|||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
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Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
              ||||||   |||   |||||'|||||||||   |||||||||| |||||||:::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
              ||||||||||||   |||||||||||||||||||||||||||,|||:::|||||.|||:|
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
              ||||||   ||||||||:|||||:::|||||   :::|||:::|||||||||'|||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
              ||||||||||||||||||||||||||||||||||'||||||||||||||||:::|||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              ||||||||||||'||||.|||||   |||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              ||||||   |||||||||||||||||||||||||||||||||:::|||   |||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
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Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              ||||||   |||||||||||||||   :::|||   ||||||||||:::|||||.||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||   ||||||||||||   |||   |:|||||:|:::::|||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
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Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              ||||||||||||||||   :::|||||||||||:::|||||||:::|||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
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Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 7
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
;  GENERAL INFORMATION:
;    APPLICANT:  Van Loon, Adolphus
;    APPLICANT:  Mitchell, David
;    TITLE OF INVENTION:  POLYPEPTIDES WITH PHYTASE ACTIVITY
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/744,231
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/424,757
;      FILING DATE:  18-APR-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;      REFERENCE/DOCKET NUMBER:  Case Docket 9339
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-2363
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  465 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  104
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  119
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  205
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  228
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  337
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  374
;      OTHER INFORMATION:  /note="potential N-glycosylation site"
US-08-744-231-33

Alignment Scores:
Pred. No.:              6.6e-173        Length:          465
Score:                  1902.00         Matches:         360
Percent Similarity:     85.01%          Conservative:    37
Best Local Similarity:  77.09%          Mismatches:      68
Query Match:            75.33%          Indels:          2
DB:                     4               Gaps:            2

US-09-488-265B-25 (1-1426) x US-08-744-231-33 (1-465)

Qy          12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
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Db           1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
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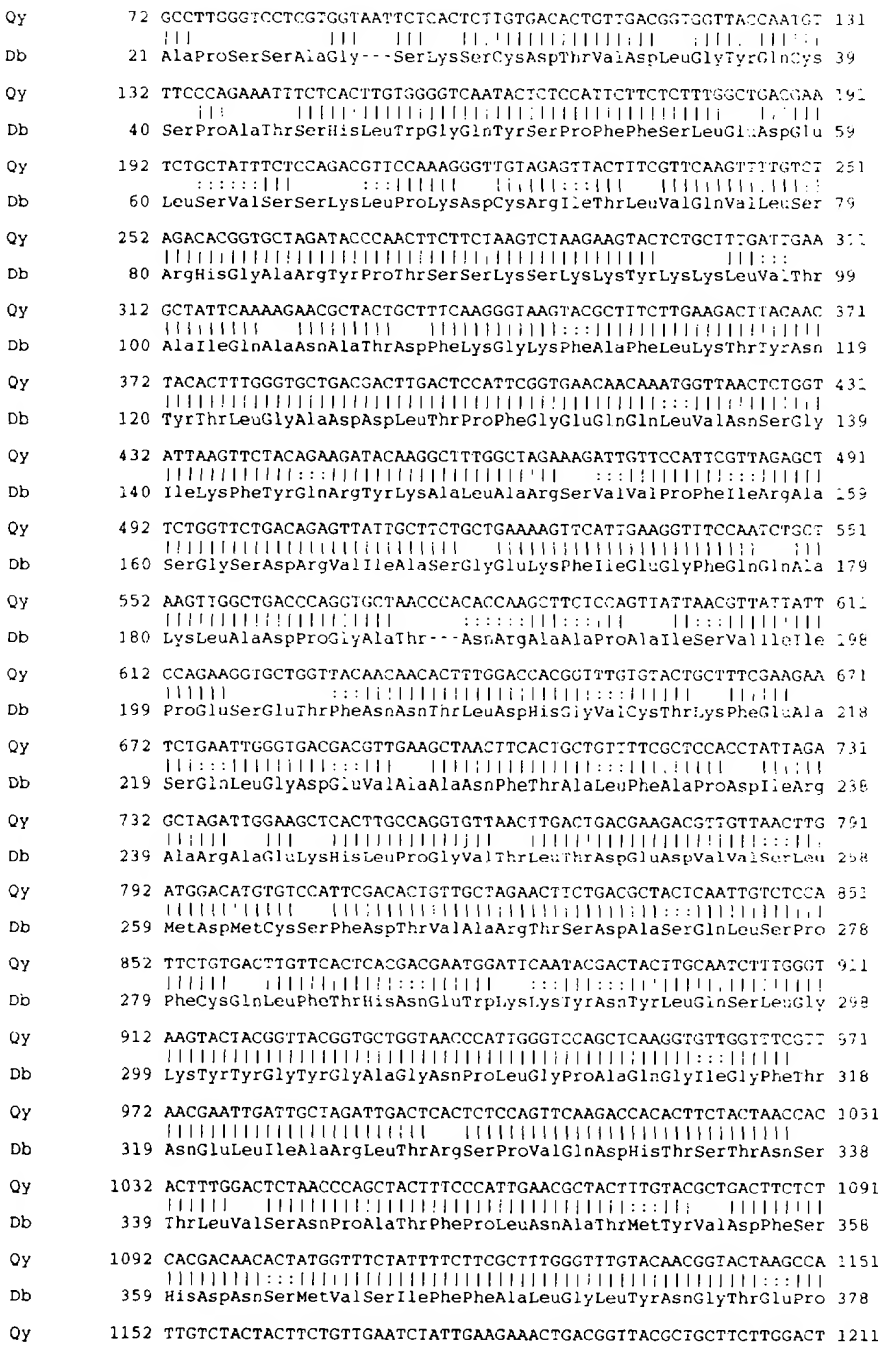

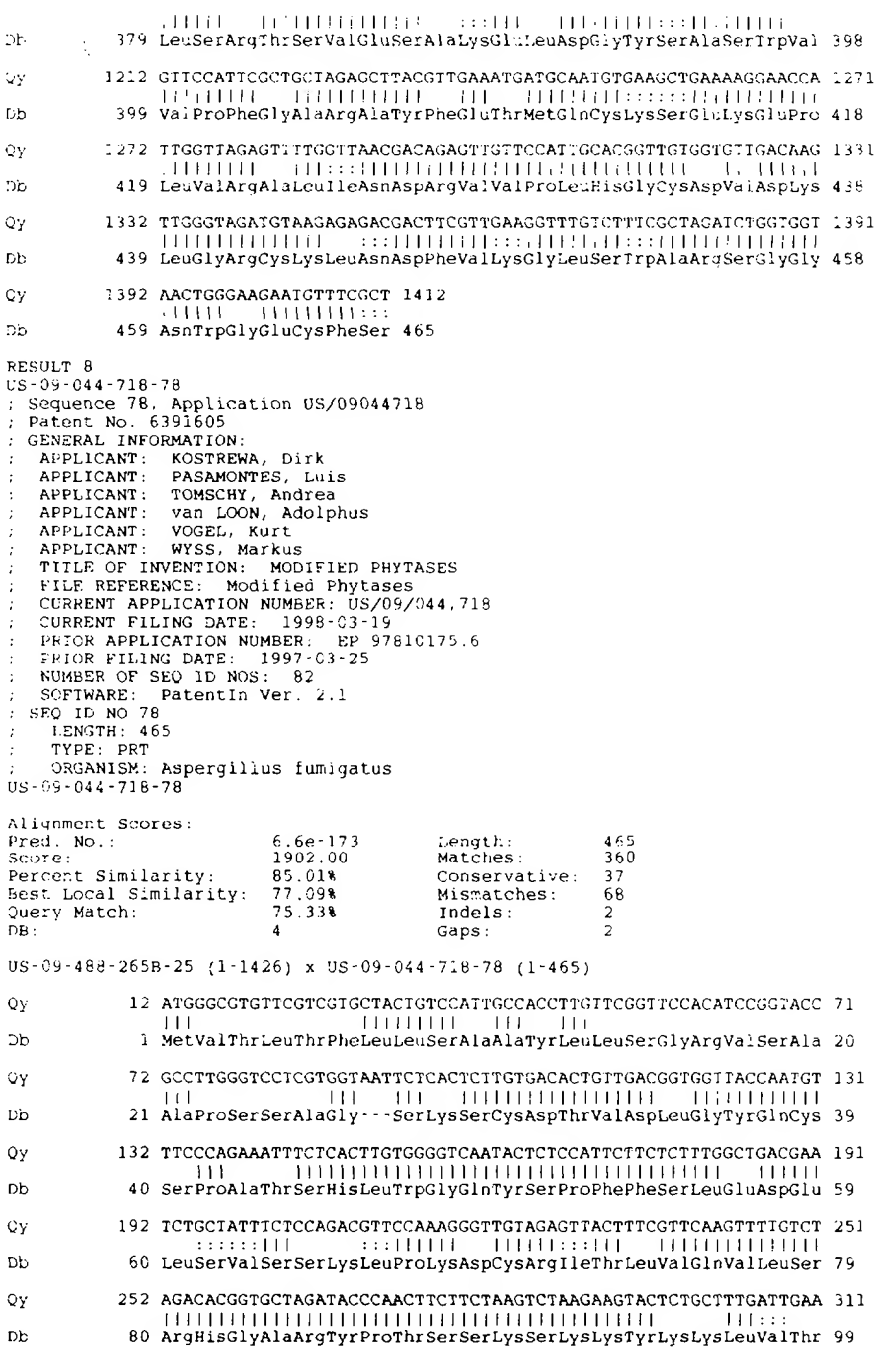

RESULT 8
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-78

Alignment Scores:

Pred. No.:	6.6e-173	Length:	465
Score:	1902.00	Matches:	360
Percent Similarity:	85.01%	Conservative:	37
Best Local Similarity:	77.09%	Mismatches:	68
Query Match:	75.33%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-25 (1-1426) x US-09-044-718-78 (1-465)

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Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              |||             |||   |||   ||||||||||||||||||   ||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
              |||      ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
              ||||||||||      |||||||||   ||||||||||   ||||||||||||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
              ||||||||||   ||||||||||   ||||||||||||||||||||||||||||||||||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
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Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
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Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
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Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
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Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

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Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTGTTTCGCTACATCTGGTGGT 1391
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Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

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Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
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Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGGTCCACCTATTAGA 731
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Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
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Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

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Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
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Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
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Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
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Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
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Db        459 AsnTrpGlyGluCysPheSer 465
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RESULT 9
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Sa
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/09/636,499
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Alignment Scores:

Pred. No.:	6.6e-173	Length:	465
Score:	1902.00	Matches:	360
Percent Similarity:	85.01%	Conservative:	37
Best Local Similarity:	77.09%	Mismatches:	68
Query Match:	75.33%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-25 (1-1426) x US-09-636-499-6 (1-465)

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Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
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Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 10
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
;  APPLICANT:  Svendsen, Allan
;  TITLE OF INVENTION:  Phytase Variants
;  FILE REFERENCE:  5618.500-US
;  CURRENT APPLICATION NUMBER: US/09/273,871A
;  CURRENT FILING DATE:  1999-03-22
;  PRIOR APPLICATION NUMBER:  PA 1998 00407
;  PRIOR FILING DATE:  1998-03-23
;  PRIOR APPLICATION NUMBER:  PA 1998 00806
;  PRIOR FILING DATE:  1998-06-19
;  PRIOR APPLICATION NUMBER:  PA 1998 01176
;  PRIOR FILING DATE:  1998-09-18
;  PRIOR APPLICATION NUMBER:  PA 1999 00091
;  PRIOR FILING DATE:  1999-01-22
;  PRIOR APPLICATION NUMBER:  60/080,129
;  PRIOR FILING DATE:  1998-03-31
;  PRIOR APPLICATION NUMBER:  60/090,675
;  PRIOR FILING DATE:  1998-06-25
;  NUMBER OF SEQ ID NOS:  15
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-273-871A-8

Alignment Scores:
Pred. No.:                6.6e-173        Length:          465
Score:                    1902.00         Matches:         360
Percent Similarity:       85.01%          Conservative:    37
Best Local Similarity:    77.09%          Mismatches:      68
Query Match:              75.33%          Indels:          2
DB:                       4               Gaps:            2

US-09-488-265B-25 (1-1426) x US-09-273-871A-8 (1-465)

Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGGTGACGAA 191
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
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```
RESULT 11
US-09-044-716-80
; Sequence 80, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
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US-09-044-716-80

Alignment Scores:

Pred. No.:	3.83e-172	Length:	465
Score:	1894.00	Matches:	359
Percent Similarity:	84.80%	Conservative:	37
Best Local Similarity:	76.87%	Mismatches:	69
Query Match:	75.01%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-25 (1-1426) x US-09-044-716-80 (1-465)

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Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              ||||||||||||||||||.|||||   ||||.||||||||| ||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              ||||||   ||||||||||||||||||||||||||||||||||||||||   ||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
              |||||||||:::|||||||||||||||||||||||||||||||||||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              ||||||   ||||||||||||||   :::|||   |||||||||:::|||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||   |||||||||||||   |||   |||||:|||:::::::|||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              |||||||||   |||:::|||||||||||||||||||||||||||||||   |||||||.|
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              ||||||||||||||   :::||||||||||:::|:|||||||:::|||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
              ||||||   ||||:|||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 12
US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-79

Alignment Scores:
Pred. No.:              4.77e-172       Length:         465
Score:                  1893.00         Matches:        359
Percent Similarity:     84.80%          Conservative:   37
Best Local Similarity:  76.87%          Mismatches:     69
Query Match:            74.97%          Indels:         2
DB:                     4               Gaps:           2

US-09-488-265B-25 (1-1426) x US-09-044-718-79 (1-465)

Qy          12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
               |||              |||||||||   |||   |||
Db           1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy          72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
               |||            |||   |||   |||||||| |||||||||   ||||.||||||
Db          21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy         132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
               |||       |.||||||||||||.|||||.|||||||||||||||||.   ||||||
Db          40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59

Qy         192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
               ::::::|||      :::||||||   ||||||:::|||   ||||||||||||||
Db          60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy         252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
               ||||||||||||||||||||||||||||||||||||||||||||||||      ||:::
Db          80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy         312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
               ||||||||   |||||||||   ||||||||||||:::|||||||||||||||||||||
Db         100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy         372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
               |||||||||||||||||:|||||:|||||||||||:|||||:|||||||||||||||||
Db         120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy         432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
               ||||||||||||:::|||||||||||||||||||||   :::|||||||||:::|:|||
Db         140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy         492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
               ||||||||||||||||||||||||||   |||||||||||||||||||||||   |||
Db         160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy         552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
               ||||||||||||||||||||||      :::::|||||:::|||   |:|:::|||||||
Db         180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy         612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
               ||||||          :::|||||||||||||||||||:::|||||   ||||||
Db         199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy         672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
               ||:::||||||||||:::|||   |||||||||||||:::|||||||   ||||||
Db         219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy         732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
               ||||||   |||   |||||||||||||||   |||||||||||||||||||||:::|||
Db         239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy         792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
               ||||||||||||   |||||||||||||||||||||||||||||||:::|||||:|||||
Db         259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy         852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
               ||||||   ||||||||||||:::||||||   :::|||:::|||||||||:|||||||
Db         279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy         912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
               ||||||||||||:|||||||||||||||||||||||:|||||||||||||:::|||||
Db         299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy         972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
               ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db         319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy        1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
               ||||||   ||||||||||||||||||||||||||||||||||:::|||   ||||||||
Db         339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy        1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
               |||||||||:::|||||||||||||||||||||||||||||||||||||||||||:::
Db         359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378
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Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 13
US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Alignment Scores:
Pred. No.:              5.14e-172       Length:         439
Score:                  1892.50         Matches:        352
Percent Similarity:     88.41%          Conservative:   37
Best Local Similarity:  80.00%          Mismatches:     50
Query Match:            74.95%          Indels:         1
DB:                     4               Gaps:           1

US-09-488-265B-25 (1-1426) x US-09-044-718-3 (1-439)

Qy         93 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 152
Db          1 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 20

Qy        153 TGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGTT 212
Db         21 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 40

Qy        213 CCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 272
Db         41 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 60

Qy        273 ACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 332
Db         61 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 80

Qy        333 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 392
Db         81 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 100

Qy        393 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 452
Db        101 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 120

Qy        453 AAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTATT 512
Db        121 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 140

Qy        513 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTGCT 572
Db        141 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 160

Qy        573 AACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAAC 632
Db        161 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 179

Qy        633 AACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTT 692
Db        180 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 199

Qy        693 GAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTG 752
Db        200 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 219

Qy        753 CCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGAC 812
Db        220 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 239

Qy        813 ACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACTCAC 872
Db        240 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 259

Qy        873 GACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCT 932
Db        260 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 279

Qy        933 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTG 992
Db        280 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 299

Qy        993 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1052
Db        300 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 319

Qy       1053 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTCT 1112
Db        320 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 339

Qy       1113 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTTGAA 1172
Db        340 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 359

Qy       1173 TCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1232
Db        360 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 379

Qy       1233 TACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1292
Db        380 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 399

Qy       1293 GACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1352
Db        400 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 419

Qy       1353 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGCT 1412
Db        420 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 439

RESULT 14
US-09-044-718-12
; Sequence 12, Application US/09044718
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; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Alignment Scores:
Pred. No.:              5.21e-172     Length:         449
Score:                  1892.50       Matches:        352
Percent Similarity:     88.41%        Conservative:   37
Best Local Similarity:  80.00%        Mismatches:     50
Query Match:            74.95%        Indels:         1
DB:                     4             Gaps:           1

US-09-488-265B-25 (1-1426) x US-09-044-718-12 (1-449)

Qy     93 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 152
Db     11 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 30

Qy    153 TGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGTT 212
Db     31 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 50

Qy    213 CCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 272
Db     51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70

Qy    273 ACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 332
Db     71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90

Qy    333 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 392
Db     91 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110

Qy    393 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 452
Db    111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130

Qy    453 AAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTATT 512
Db    131 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 150

Qy    513 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTGCT 572
Db    151 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 170

Qy    573 AACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAAC 632
Db    171 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189

Qy    633 AACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTT 692
Db    190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209

Qy    693 GAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTG 752
Db    210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 229

Qy    753 CCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGAC 812
Db    230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249

Qy    813 ACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACTCAC 872
Db    250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269

Qy    873 GACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCT 932
Db    270 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 289

Qy    933 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTG 992
Db    290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309

Qy    993 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1052
Db    310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329

Qy   1053 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTCT 1112
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Qy   1113 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTTGAA 1172
Db    350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 369

Qy   1173 TCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1232
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Qy   1233 TACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1292
Db    390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409

Qy   1293 GACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1352
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Qy   1353 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGCT 1412
Db    430 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 449

RESULT 15
US-09-044-718-81
; Sequence 81, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
;  APPLICANT:  KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION:  MODIFIED PHYTASES
;  FILE REFERENCE:  Modified Phytases
;  CURRENT APPLICATION NUMBER: US/09/044,718
;  CURRENT FILING DATE:  1998-03-19
;  PRIOR APPLICATION NUMBER:  EP 97810175.6
;  PRIOR FILING DATE:  1997-03-25
;  NUMBER OF SEQ ID NOS:  82
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Alignment Scores:
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Pred. No.:	9.22e-172	Length:	465
Score:	1890.00	Matches:	358
Percent Similarity:	84.80%	Conservative:	38
Best Local Similarity:	76.66%	Mismatches:	69
Query Match:	74.85%	Indels:	2
DB:	4	Gaps:	2

US-09-488-265B-25 (1-1426) x US-09-044-718-81 (1-465)

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Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC  71
              |||                 |||||||||   |||   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla  20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              |||           |||   |||   |||||||||||||||||   |||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys  39

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
                 |||      |||||||||||||||||||||||||||||||||||||||||||||||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu  59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
                 :::::|||      :::||||||   |||||.:::|||   |||||||||||||..
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer  79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              ||||.|||||||||||||||||||||||||||||||.|||||||||      ||||::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr  99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
              |||||||||   |||.|||||   |||||||||||.|:::|||||||||||||||||| |
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
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Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
              |||||||||||||||||||||||||||   |||.|||||.|||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
              |||||||||||||||||||||      :::::|||:::|||   |||:::|||||||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
              ||||||         :::|||||||||||||||||||||:::|'||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
              |||:::|||||||||:::|||   |||||||||||||||:::|||||||.||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
              ||||||   :::   |||||||||||||||   |||||||.|||||||||||||| ::::||
Db        239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
              ||||||||||||   |||||||||||||||||||||||||||||||:::|||||||||.|
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
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Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
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Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
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Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
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Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

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Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
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Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
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Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
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Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCCCTAGATCTGGTGGT 1391
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Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
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Db        459 AsnTrpGlyGluCysPheSer 465
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Job time : 48.3866 secs

GenCore version 5.1.6

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 08:05:37 ; Search time 71.7378 Seconds
(without alignments)
6289.894 Million cell updates/sec

Title: US-09-488-265B-25
Perfect score: 2525
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 1175308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=oct3.rapb -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2311	91.5	467	14	US-10-083-452-9	Sequence 9, Appli
2	1902	75.3	465	14	US-10-083-452-8	Sequence 8, Appli
3	1902	75.3	465	15	US-10-062-848-78	Sequence 78, Appl
4	1902	75.3	465	15	US-10-229-358-6	Sequence 6, Appli
5	1898.5	75.2	474	15	US-10-213-990-24	Sequence 24, Appl
6	1894	75.0	465	15	US-10-062-848-80	Sequence 80, Appl
7	1893	75.0	465	15	US-10-062-848-79	Sequence 79, Appl
8	1892.5	75.0	439	15	US-10-062-848-3	Sequence 3, Appli
9	1892.5	75.0	449	15	US-10-062-848-12	Sequence 12, Appl
10	1890	74.9	465	15	US-10-062-848-81	Sequence 81, Appl
11	1868	74.0	469	15	US-10-062-848-82	Sequence 82, Appl
12	1862	73.7	467	15	US-10-079-709-32	Sequence 32, Appl
13	1862	73.7	467	15	US-10-229-358-5	Sequence 5, Appli
14	1855	73.5	467	9	US-09-929-060-3	Sequence 3, Appli
15	1850	73.3	467	14	US-10-083-452-11	Sequence 11, Appl
16	1843	73.0	462	15	US-10-229-358-12	Sequence 12, Appl
17	1820	72.1	444	15	US-10-062-848-1	Sequence 1, Appli
18	1813.5	71.8	463	14	US-10-083-452-10	Sequence 10, Appl
19	1813	71.8	443	9	US-09-929-060-1	Sequence 1, Appli
20	1808	71.6	443	9	US-09-929-060-2	Sequence 2, Appli
21	1798.5	71.2	447	15	US-10-062-848-6	Sequence 6, Appli
22	1756	69.5	466	14	US-10-083-452-12	Sequence 12, Appl
23	1756	69.5	466	15	US-10-229-358-7	Sequence 7, Appli
24	1752	69.4	450	15	US-10-062-848-15	Sequence 15, Appl
25	1719	68.1	466	14	US-10-083-452-13	Sequence 13, Appl
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28	1661	65.8	489	15	US-10-229-358-4	Sequence 4, Appli
29	1661	65.8	489	15	US-10-229-358-10	Sequence 10, Appl
30	1637	64.8	410	15	US-10-229-358-11	Sequence 11, Appl
31	1395	55.2	475	14	US-10-083-452-14	Sequence 14, Appl
32	1346.5	53.3	487	14	US-10-083-452-15	Sequence 15, Appl
33	1346.5	53.3	487	15	US-10-229-358-8	Sequence 8, Appli
34	1335	52.9	355	15	US-10-229-358-15	Sequence 15, Appl
35	1222	48.4	495	14	US-10-083-452-2	Sequence 2, Appli
36	1217	48.2	478	14	US-10-083-452-3	Sequence 3, Appli
37	917	36.3	284	15	US-10-229-358-19	Sequence 19, Appl
38	880	34.9	283	15	US-10-229-358-9	Sequence 9, Appli
39	880	34.9	283	15	US-10-229-358-24	Sequence 24, Appl
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43	822	32.6	442	14	US-10-083-452-4	Sequence 4, Appli
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45	412	16.3	312	15	US-10-229-358-21	Sequence 21, Appl

ALIGNMENTS

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; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
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; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-06-25
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;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Variation
US-10-083-452-9

Alignment Scores:
Pred. No.:                2e-178          Length:          467
Score:                    2311.00         Matches:         435
Percent Similarity:       95.93%          Conservative:    13
Best Local Similarity:    93.15%          Mismatches:      19
Query Match:              91.52%          Indels:          0
DB:                       14              Gaps:            0

US-09-488-265B-25 (1-1426) x US-10-083-452-9 (1-467)

Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||   |||| |
Db         41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
              |||||||||||||||||||||      ||||||||||||||||||||||||||.||
Db         61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              |||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db         81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
              |||||||||||||||||||||||||||||||||||||||||||||||||||.|||.|||
Db        101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
              ||||||||||.|||||||||||||||||||||||.||||||   |||.|||| ||| |||
Db        121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
              |||||||||||||||||| ||||| |||||||||||.|||||||||||:::.|||.|
Db        141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
              ||||||||||.|||||||||||||||||||||||||.|||.||||||||||||||||.||
Db        161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
              ||:|||||||||||||:::   ||:||||,|||||||||||||:::|||:||||||
Db        181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleIle 200

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
              |||||||||:::|||||||||||||||||||||||||||||   ||||||||||.||.:::
Db        201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
              |||||||||||||||||||||||||||||||||||||||:::|||||||||   ||||||
Db        221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
              ||||||||||||||   ||||||||||||   ||||||||||||||||||||   :||
Db        241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
              |:|||||   |||||:|||||||||||||||||   |||||||||:|||||||||||||
Db        281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
              ||||||||||||.|||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              |||||||||||||||:|||||||||   ||||||||||||||||||||||||||||||||
Db        321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
              ||||||||||:::|||||:|||||||||||||||||||||||||||||||||   |||
Db        361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
Db        381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||   ||||||||||||||||||||||||||||||:::|||||||||||||||
Db        401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              |||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
              ||||||   |||||||.||||
Db        461 AsnTrpAlaGluCysPheAla 467

RESULT 2
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
;  APPLICANT: Svendsen, Allan
;  TITLE OF INVENTION: Phytase Variants
;  FILE REFERENCE: 5618.500-US
;  CURRENT APPLICATION NUMBER: US/10/083,452
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: US/09/273,871
;  PRIOR FILING DATE: 1999-03-22
;  PRIOR APPLICATION NUMBER: PA 1998 00407
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: PA 1998 00806
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: PA 1998 01176
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: PA 1999 00091
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/080,129
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/090,675
;  PRIOR FILING DATE: 1998-06-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
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US-10-083-452-8

Alignment Scores:

Pred. No.:	2.46e-145	Length:	465
Score:	1902.00	Matches:	360
Percent Similarity:	85.01%	Conservative:	37
Best Local Similarity:	77.09%	Mismatches:	68
Query Match:	75.33%	Indels:	2
DB:	14	Gaps:	2

US-09-488-265B-25 (1-1426) x US-10-083-452-8 (1-465)

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Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
              ||'                 |||:||||   | |   |||
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              |||           |||  |||  ||||||||||||||||   ||||||||||
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 33

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
                 |||      |||||||||||||||||||||||||,||||,|||||||||||   |||:||
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
              :::::::|||      :::||||||   |||||':::|||   ||||:|||||||||
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              |||||||||||||||||||:|||:|||||||||||||||||||   '| :::
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
              |||||||||   |||:|||||   ||||||||||||:::|||||.|||||,||||:|||
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
              |||||||||||:::|||||||||||||||||||||;   :::||||||:|||:::||||||
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
              |||||||||||||||||||||||||'   |||||||||||||||||||||||   |||
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
              ||||:|||||||||||||||      ::::::|||:::|||   ||||::|||:|||||
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
              ||||||         :::|||||||||||||||||||:::|||||   ||||||
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
              |||:::|||||||||:::|||   |||||||||||||||:::|||||||||   ||||||
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
              ||||||   |||   |||||||||||||||   ||| ||||||||||||||| :::|||
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTGTCCA 851
              ||||||||||||   |||||||||||||||||||'||||||||:::|||.|||||||
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
              ||||||   ||||||||||':::|||||   :::.||:::: ||||||||||'|||.'
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
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                .||||||||||||||||||:||||||||||||:||||||||||||-||||:::|:||||
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 316

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              '|||||   ||||||||||||||||.|||||.|||||||||:::|||   ||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
              |||'||||||:::||||:|||||'|||||||||||||||||||||,||||||||||:::|||
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              ||||||   ||||.|||||||||   ::::||   ||||||||:::||||||||
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||   ||||:|||||||   |||   ||||||||.:::::::|:|||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              ||||||||||   ||.:::|||||||||||||||||:|||||||||||:|   ||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              |||||||||||||||||   :::||||||||:::|||||||||||||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
              ||||||   ||||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 3
US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-78
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Alignment Scores:

Pred. No.:	2.46e-145	Length:	465
Score:	1902.00	Matches:	360
Percent Similarity:	85.01%	Conservative:	37
Best Local Similarity:	77.09%	Mismatches:	68
Query Match:	75.33%	Indels:	2
DB:	15	Gaps:	2

US-09-488-265B-25 (1-1426) x US-10-062-848-78 (1-465)

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Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
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Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 196

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
Db        339 ThrLeuValSerAsnProAlaThrProProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 4
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Sam
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Alignment Scores:
Pred. No.:                2.46e-145       Length:          465
Score:                    1902.00         Matches:         360
Percent Similarity:       85.01%          Conservative:    37
Best Local Similarity:    77.09%          Mismatches:      68
Query Match:              75.33%          Indels:          2
DB:                       15              Gaps:            2

US-09-488-265B-25 (1-1426) x US-10-229-358-6 (1-465)

Qy          12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
Db           1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy          72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
Db          21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy         132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
Db          40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy         192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
Db          60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy         252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
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Db        80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy       312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
Db       100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy       372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
Db       120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy       432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
Db       140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy       492 TCTGGTTCTCACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
Db       160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy       552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
Db       180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 196

Qy       612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
Db       199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy       672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db       219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy       732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
Db       239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy       792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
Db       259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy       852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
Db       279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy       912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
Db       299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy       972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
Db       319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy      1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
Db       339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy      1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
Db       359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy      1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
Db       379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy      1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
Db       399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy      1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
Db       419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy      1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
Db       439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy      1392 AACTGGGAAGAATGTTTCGCT 1412
Db       459 AsnTrpGlyGluCysPheSer 465

RESULT 5
US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Bo
;  APPLICANT:  Bussey, Howard
;  APPLICANT:  Storms, Reg
;  APPLICANT:  Roemer, Terry
;  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
;  TITLE OF INVENTION:  ENZYMES AND METHODS OF USE
;  FILE REFERENCE: 10182-019-999
;  CURRENT APPLICATION NUMBER: US/10/213,990
;  CURRENT FILING DATE:  2002-08-05
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 474
;   TYPE: PRT
;   ORGANISM: Aspergillus
US-10-213-990-24

Alignment Scores:
Pred. No.:              4.76e-145       Length:         474
Score:                  1898.50         Matches:        357
Percent Similarity:     84.89%          Conservative:   42
Best Local Similarity:  75.95%          Mismatches:     64
Query Match:            75.19%          Indels:         7
DB:                     15              Gaps:           2

US-09-488-265b-25 (1-1426) x US-10-213-990-24 (1-474)

Qy          3 TATGAATTCATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACA 62
Db         12 TyrLeuLeuSerGlyAlaValValLeuIleLeuLysArgSerArgValSerAlaAlaPro 31

Qy         63 TCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGT 122
Db         32 SerSer----------------AlaGlySerLysSerCysAspThrValAspLeuGly 45

Qy        123 TACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTG 182
Db         46 TyrGlnCysSerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeu 65

Qy        183 GCTGACGAATCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAA 242
Db         66 GluAspGluLeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGln 85

Qy        243 GTTTTGTCTAGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCT 302
Db         86 ValLeuSerArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLys 105

Qy        303 TTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAG 362
Db        106 LeuValThrAlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLys 125

Qy        363 ACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTT 422
Db        126 ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuVal 145

Qy        423 AACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTC 482
Db        146 AsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPhe 165

Qy        483 GTTAGAGCTTCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTC 542
Db        166 IleArgAlaSerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPhe 185
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Qy        543 CAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC 602
Db        186 GlnGlnAlaLysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSer 204

Qy        603 GTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCT 662
Db        205 ValIleIleProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLys 224

Qy        663 TTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCA 722
Db        225 PheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaPro 244

Qy        723 CCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTT 782
Db        245 AspIleArgAlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspVal 264

Qy        783 GTTAACTTGATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAA 842
Db        265 ValSerLeuMetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGln 284

Qy        843 TTGTCTCCATTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAA 902
Db        285 LeuSerProPheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGln 304

Qy        903 TCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTT 962
Db        305 SerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIle 324

Qy        963 GGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCT 1022
Db        325 GlyPheThrAsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSer 344

Qy       1023 ACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCT 1082
Db        345 ThrAsnSerThrLeuValSerAsnProAlaThrProProLeuAsnAlaThrMetTyrVal 364

Qy       1083 GACTTCTCTCACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGT 1142
Db        365 AspPheSerHisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGly 384

Qy       1143 ACTAAGCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCT 1202
Db        385 ThrGluProLeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAla 404

Qy       1203 TCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAA 1262
Db        405 SerTrpValValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlu 424

Qy       1263 AAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGT 1322
Db        425 LysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAsp 444

Qy       1323 GTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGA 1382
Db        445 ValAspLysLeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArg 464

Qy       1383 TCTGGTGGTAACTGGGAAGAATGTTTCGCT 1412
Db        465 SerGlyGlyAsnTrpGlyGluCysPheSer 474

RESULT 6
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-80

Alignment Scores:
Pred. No.:                1.09e-144       Length:          465
Score:                    1894.00         Matches:         359
Percent Similarity:       84.80%          Conservative:    37
Best Local Similarity:    76.87%          Mismatches:      69
Query Match:              75.01%          Indels:          2
DB:                       15              Gaps:            2

US-09-488-265B-25 (1-1426) x US-10-062-848-80 (1-465)

Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGCTAGAGCT 491
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
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Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1092 CACGACAACACTATGGTTTCTATTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCCCT 1412
Db        459 AsnTrpGlyGluCysPheSer 465
```

RESULT 7
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-79

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Alignment Scores:
Pred. No.:               1.32e-144     Length:         465
Score:                   1893.00       Matches:        359
Percent Similarity:      84.80%        Conservative:   37
Best Local Similarity:   76.87%        Mismatches:     69
Query Match:             74.97%        Indels:         2
DB:                      15            Gaps:           2

US-09-488-265B-25 (1-1426) x US-10-062-848-79 (1-465)

Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
Db          1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
Db         21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
Db         40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu 59

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
Db         60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
Db         80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
Db        100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
Db        120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
Db        140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
Db        160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
Db        180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
Db        199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db        219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
Db        239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
Db        259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
Db        279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
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Db        299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db        319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              ||||||   ||||||||||||||||||||||||||||||||||||:|||   ||||||||
Db        339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
              |||||||||:::||||||||||||||||||||||||||||||||||||||||||||:::
Db        359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              ||||||   ||||||||||||||   :::|||   |||:|||||:::||||||||:|
Db        379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||   ||||||||||||   |||   |||||||||:::::||||||||||||
Db        399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy       1272 ITGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              |||||||||   |||:::||||||||||||||||||||||||||||||   ||||||||||
Db        419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              |||||||||||||||   :::||||||||||:::||||:||||:::||||||||||||||
Db        439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
              ||||||   ||||||||:::
Db        459 AsnTrpGlyGluCysPheSer 465

RESULT 8
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-3

Alignment Scores:
Pred. No.:              1.41e-144       Length:         439
Score:                  1892.50         Matches:        352
Percent Similarity:     88.41%          Conservative:   37
Best Local Similarity:  80.00%          Mismatches:     50
Query Match:            74.95%          Indels:         1
DB:                     15              Gaps:           1

US-09-488-265B-25 (1-1426) x US-10-062-848-3 (1-439)

Qy          93 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 152
               |||   ||||||||||||||||||   ||||||||||||   |||      |||||||||

Db           1 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 20

Qy         153 TGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGTT 212
               ||||||||||||||||||||||||||||||||   ||||||   :::::|||      :::
Db          21 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 40

Qy         213 CCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 272
               ||||||   ||||||:::|||   |||||||||||||||||||||||||||||||||||
Db          41 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 60

Qy         273 ACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 332
               ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 80

Qy         333 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 392
               ||||||||||||:::|||||||||:|||||||||||||||||||||||||||||||||||
Db          81 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 100

Qy         393 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 452
               |||||||||||||||||||||||:::|||||||||||||||||||||||||||:::||||||
Db         101 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 120

Qy         453 AAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACACAGTTATT 512
               ||||||||||||||   :::|||||||||:::|||||||||||||||||||||||||||||
Db         121 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 140

Qy         513 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTGCT 572
               ||||||   ||||||||||||||||||||||   ||||||||||||||||||||||||||
Db         141 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 160

Qy         573 AACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAAC 632
                     ::::::||:::|||   |||:::||||||||||||||||          :::|||
Db         161 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 179

Qy         633 AACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTT 692
               ||||||||||||||||:::||||||   ||||||   ||||:::|||||||||:::|||
Db         180 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 199

Qy         693 GAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTG 752
                  ||||||||||||||:::|||||||||   ||||||||||||   |||   ||||||
Db         200 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 219

Qy         753 CCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGAC 812
               |||||||||   |||||||||||||||||||:::|||||||||||||||||   ||||:|
Db         220 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 239

Qy         813 ACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACTCAC 872
               ||||||||||||||||||||||:::|||||||||||||||||||   ||||||||||||
Db         240 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 259

Qy         873 GACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCT 932
               ::||||||   :::|||:::||||||||||||||||||||||||||||||||||||||||
Db         260 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 279

Qy         933 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTG 992
               ||||||||||||||||||||||||||:::||||||   ||||||||||||||||||:|
Db         280 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 299

Qy         993 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1052
               |||   ||||||||||||||||||||||||||||||||||   ||||  |||||||||||
Db         300 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 319

Qy        1053 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTCT 1112
               ||||||||||||||||||||||:::|||   ||||||||||||||||||:::||||||||
Db         320 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 339

Qy        1113 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTTGAA 1172
               ||||||||||||||||||||||||||||||||||:::|||||||   ||||||||||||
Db         340 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 359

Qy        1173 TCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1232
               |||   :::|||   |||||||||:::|||||||||   |||||||||   |||||||||
Db         360 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 379
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Qy       1233 TACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1292
Db        380 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 399

Qy       1293 GACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1352
Db        400 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 419

Qy       1353 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGCT 1412
Db        420 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 439

RESULT 9
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Alignment Scores:
Pred. No.:                1.43e-144       Length:          449
Score:                    1892.50         Matches:         352
Percent Similarity:       88.41%          Conservative:     37
Best Local Similarity:    80.00%          Mismatches:       50
Query Match:              74.95%          Indels:            1
DB:                       15              Gaps:              1

US-09-488-265B-25 (1-1426) x US-10-062-848-12 (1-449)

Qy         93 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCCAGAAATTTCTCACTTG 152
Db         11 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 30

Qy        153 TGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAATCTGCTATTTCTCCAGACGTT 212
Db         31 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 50

Qy        213 CCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCTAGACACGGTGCTAGATACCCA 272
Db         51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70

Qy        273 ACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAAGCTATTCAAAAGAACGCTACT 332
Db         71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90

Qy        333 GCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 392
Db         91 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110

Qy        393 TTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGTATTAAGTTCTACAGAAGATAC 452
Db        111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130

Qy        453 AAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCTTCTGGTTCTGACAGAGTTATT 512
Db        131 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 150

Qy        513 GCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCTAAGTTGGCTGACCCAGGTGCT 572
Db        151 AlaSerGlyGluLysPheIleGluGlyPheGluGlnAlaLysLeuAlaAspProGlyAla 170

Qy        573 AACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATTCCAGAAGGTGCTGGTTACAAC 632
Db        171 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189

Qy        633 AACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAATCTGAATTGGGTGACGACGTT 692
Db        190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209

Qy        693 GAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCACTTG 752
Db        210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 229

Qy        753 CCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTGATGGACATGTGTCCATTCGAC 812
Db        230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249

Qy        813 ACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCATTCTGTGACTTGTTCACTCAC 872
Db        250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269

Qy        873 GACGAATGGATTCAATACGACTACTTGCAATCTTTGGGTAAGTACTACGGTTACGGTGCT 932
Db        270 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 289

Qy        933 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTTAACGAATTGATTGCTAGATTG 992
Db        290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309

Qy        993 ACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCACACTTTGGACTCTAACCCAGCT 1052
Db        310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329

Qy       1053 ACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACAACACTATGGTTTCT 1112
Db        330 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 349

Qy       1113 ATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCATTGTCTACTACTTCTGTTGAA 1172
Db        350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 369

Qy       1173 TCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACTGTTCCATTCGCTGCTAGAGCT 1232
Db        370 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 389

Qy       1233 TACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTGGTTAGAGTTTTGGTTAAC 1292
Db        390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409

Qy       1293 GACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAGTTGGGTAGATGTAAGAGAGAC 1352
Db        410 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 429

Qy       1353 GACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGAATGTTTCGCT 1412
Db        430 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 449

RESULT 10
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
```

```
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
;   LENGTH: 465
;   TYPE: PRT
;   ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Alignment Scores:
Pred. No.:                2.3e-144      Length:          465
Score:                    1890.00       Matches:         358
Percent Similarity:       84.80%        Conservative:    38
Best Local Similarity:    76.66%        Mismatches:      69
Query Match:              74.85%        Indels:          2
DB:                       15            Gaps:            2

US-09-488-265B-25 (1-1426) x US-10-062-848-81 (1-465)

Qy          12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
               |||                 |||||||||   |||   |||
Db           1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

Qy          72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
               |||          |||   |||   ||||||||||||||||||   ||||||||||||
Db          21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

Qy         132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
                  |||      ||||||||||||||||||||||||||||||||||||||||   ||||||
Db          40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

Qy         192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
                  :::::|||      :::||||||   ||||||:::|||   ||||||||||||||
Db          60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79

Qy         252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
               |||||||||||||||||||||||||||||||||||||||||||||||      ||||:::
Db          80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99

Qy         312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
               |||||||||   |||||||||   ||||||||||:::|||||||||||||||||:::|||
Db         100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119

Qy         372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
               ||||||||||:|||||:|||||||||||   :||| ||||||||||:::|||||||||| |
Db         120 TyrThrLeuGlyAlaAspAspLeuThrAlaPheGlyGluGlnGlnLeuValAsnSerGly 139

Qy         432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
               ||||||||||:|||:::|||||||||||||||||||||   :::|||||||||:::|||||
Db         140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

Qy         492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
               ||||||||||||||||||||||||||||   |||||.|||||||||||:|||||:   : |
Db         160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179

Qy         552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
               ||||||||||||||||||||      :::::::|||:::|||   |||:::|||||||||
Db         180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

Qy         612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
               ||||||         :::|||||||||||||||||||:::||||||   ||||||
Db         199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 216

Qy         672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
               |.|:::|||||||||:|:::|||   ||||||||||||||:|::|||||||||   ||||||
Db         219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

Qy         732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
               ||||||   :::   ||||||||||||||||   ||||||||||||||||||||:::|||
Db         239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

Qy         792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
               .||||||||||   |||||||||||||||||||||||||||||||:::|||||||||||
Db         259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

Qy         852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
               ||||||   ||||||||||||:::|||||   :::|||:::|||||||||||||||||
Db         279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

Qy         912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
               ||||||||||||||||||||||||||||||||||||||||||||||:::|||   |||||
Db         299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

Qy         972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
               ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db         319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

Qy        1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
               ||||||   ||||||||||||||||||||||||||||||||||||:::|||   ||||:|||
Db         339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

Qy        1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
               |||:||||||:::|||||||||||||||||||||||||||||||||||||||||:::|||
Db         359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

Qy        1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
               ||||||   |||||||||||||||   :::|||   ||||||||||:::||||||||
Db         379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398

Qy        1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
               ||||||||||   |||||||||||   |||   |||||||||:::::|||||||||||
Db         399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

Qy        1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
               |||||||||   |||:::|||||||||||||||||||||||||||||||||   |||||||||
Db         419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

Qy        1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
               ||||||||||||||   :::||||||||:::|||||||||:::||||||||||||||||
Db         439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

Qy        1392 AACTGGGAAGAATGTTTCGCT 1412
               ||:|||   ||||||||||:::
Db         459 AsnTrpGlyGluCysPheSer 465

RESULT 11
US-10-062-848-82
; Sequence 82, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
;  APPLICANT: KOSTREWA, Dirk
;  APPLICANT:  PASAMONTES, Luis
;  APPLICANT:  TOMSCHY, Andrea
;  APPLICANT:  van LOON, Adolphus
;  APPLICANT:  VOGEL, Kurt
;  APPLICANT:  WYSS, Markus
;  TITLE OF INVENTION: MODIFIED PHYTASES
;  FILE REFERENCE: Modified Phytases
;  CURRENT APPLICATION NUMBER: US/10/062,848
;  CURRENT FILING DATE:  2002-02-01
;  PRIOR APPLICATION NUMBER: 09/044,718
;  PRIOR FILING DATE: 1998-03-19
;  PRIOR APPLICATION NUMBER: EP 97810175.6
;  PRIOR FILING DATE: 1997-03-25
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 82
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-82

Alignment Scores:

Pred. No.:	1.39e-142	Length:	469
Score:	1868.00	Matches:	348
Percent Similarity:	85.11%	Conservative:	52
Best Local Similarity:	74.04%	Mismatches:	66
Query Match:	73.98%	Indels:	4
DB:	15	Gaps:	2

US-09-488-265B-25 (1-1426) x US-10-062-848-82 (1-469)

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Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGT--- 68
              |||||||           |||||||||:::      |||           :::|||
Db          1 MetGlyAlaLeuThrPheLeuLeuSerValMetTyrLeuLeuGlyValAlaGlyAla 20

Qy         69 ------ACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGT 122
                    :::                      |||   :::|||||||||||:::   :||
Db         21 ProSerSerGlyCysSerAlaGlySerGlySerLysAlaCysAspThrValGluLeuGly 40

Qy        123 TACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCCTTTG 182
              |||||||||   |||      |||||||||||||||||||||||||||| |||.|||||
Db         41 TyrGlnCysSerProGlyThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeu 60

Qy        183 GCTGACGAATCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAA 242
              ||||||   :::::::||   |||:::|||||   |||||||||||||||| |||
Db         61 GluAspGluLeuSerValSerSerAspLeuProLysAspCysArgValThrPheValGln 80

Qy        243 GTTTTGTCTAGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCT 302
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db         81 ValLeuSerArgHisGlyAlaArgTyrProThrAlaSerLysSerLysLysTyrLysLys 100

Qy        303 TTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAG 362
              |||:::   |||||||||||||||||||   ||||||||||:::|||||| ||| :::
Db        101 LeuValThrAlaIleGlnLysAsnAlaThrGluPheLysGlyLysPheAlaPheLeuGlu 120

Qy        363 ACTTACAACTACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTT 422
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnMetVal 140

Qy        423 AACTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTC 482
              |||||||||||||||||||:::::|||||||||||||||||   :::||||||||||
Db        141 AsnSerGlyIleLysPheTyrGlnLysTyrLysAlaLeuAlaGlySerValValProPhe 160

Qy        483 GTTAGAGCTTCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTC 542
              :::|||:::|||||||||||||||||||||||||   ||||||||.||||||||||||
Db        161 IleArgSerSerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPhe 180

Qy        543 CAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAC 602
              |||   |||   :::|||:|.|||||||      :::::|||:::||,|||||:::
Db        181 GlnGlnAlaAsnValAlaAspProGlyAlaThr---AsnArgAlaAlaProValIleSer 199

Qy        603 GTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCT 662
              ||||||||||||||         |||||||||||||||||||   :::|||||,|
Db        200 ValIleIleProGluSerGluThrTyrAsnAsnThrLeuAspHisSerValCysThrAsn 219

Qy        663 TTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCA 722
              ||||||   |||||||||:|||||:::|||||||||||||||||||||:::|||||||,
Db        220 PheGluAlaSerGluLeuGlyAspGluValGluAlaAsnPheThrAlaLeuPheAlaPro 239

Qy        723 CCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTT 782
              ||||||||||||:::|||   ||||||||||||||   |||||||||:::||||||
Db        240 AlaIleArgAlaArgIleGluLysHisLeuProGlyValGlnLeuThrAspAspAspVal 259

Qy        783 GTTAACTTGATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAA 842
              |||:::|||||||||||||||   |||||||||||||||||||:::||||||:::::
Db        260 ValSerLeuMetAspMetCysSerPheAspThrValAlaArgThrAlaAspAlaSerGlu 279

Qy        843 TTGTCTCCATTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAA 902
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 LeuSerProPheCysAlaIlePheThrHisAsnGluTrpLysLysTyrAspTyrLeuGln 299

Qy        903 TCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTT 962
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||:|:::
Db        300 SerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIle 319

Qy        963 GGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCT 1022
              ||||||   |||||||||||||||:|||||||||:::|||||||'|||||||||||||
Db        320 GlyPheThrAsnGluLeuIleAlaArgLeuThrAsnSerProValGlnAspHisThrSer 339

Qy       1023 ACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCT 1082
              ||||||   |||||||||||||:::|||||||||||||||||||||||||:|||:::|||
Db        340 ThrAsnSerThrLeuAspSerAspProAlaThrPheProLeuAsnAlaThrIleTyrVal 359

Qy       1083 GACTTCTCTCACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGT 1142
              |||||||||||||||||   |||:::   |||||||||||||:::|||||||||||||||
Db        360 AspPheSerHisAspAsnGlyMetIleProIlePhePheAlaMetGlyLeuTyrAsnGly 379

Qy       1143 ACTAAGCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCT 1202
              |||:::|||||||||   ||||||   ||||||   :::|||:::::::|||||:::|||
Db        380 ThrGluProLeuSerGlnThrSerGluGluSerThrLysGluSerAsnGlyTyrSerAla 399

Qy       1203 TCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAA 1262
              ||||||   ||||||||||   ||||||||||||   |||   ||||||||||:::::|||
Db        400 SerTrpAlaValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlu 419

Qy       1263 AAGGAACCATTGGTTAGAGTTCTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGT 1322
              |||||||||||||||||   |||:::|||||||||||||||||||||||||||||||||
Db        420 LysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAla 439

Qy       1323 GTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGA 1382
              |||||||||||||.||||||||||      ||||||||:::|||||||||:::|||||||
Db        440 ValAspLysLeuGlyArgCysLysLeuLysAspPheValLysGlyLeuSerTrpAlaArg 459

Qy       1383 TCTGGTGGTAACTGGGAAGAATGTTTCGCT 1412
              ||||||||||||   |||:::   |||:::
Db        460 SerGlyGlyAsnSerGluGlnSerPheSer 469
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RESULT 12
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999

```
;      APPLICATION NUMBER:  07/688,578
;      FILING DATE:  24-MAY-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H.
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  24615-20026.00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-327-7250
;      TELEFAX:  415-327-2951
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  467 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-079-709-32

Alignment Scores:
Pred. No.:                4.24e-142      Length:          467
Score:                    1862.00        Matches:         348
Percent Similarity:       83.94%         Conservative:    44
Best Local Similarity:    74.52%         Mismatches:      75
Query Match:              73.74%         Indels:          0
DB:                       15             Gaps:            0

US-09-488-265B-25 (1-1426) x US-10-079-709-32 (1-467)

Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
              |||||||||      ||||||||   :::      |||   |||   ||||||:|||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              |||:::            |||      ||||||||||||||||||   ||||||||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
              |||   |||   ||||||:||||||||||||||:::|||||||||||||||||:::|||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
              |||   ||||||||:::|||||   ||||||||||||||:|||   ||||||||||||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              ||||||||||||||||||||:|||   ||||||   ||||||||||||||||||:|||:
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
              ||||||:::|||||||||   |||   :|||||||||||||||||||||||||||||||
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
              |||:::|||||||||:|||||||||||:|||||||||||||||||:::::::|:|||||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
              ||||||||||:::|||:|||||||||||   |||   |||||||||:|||:::|||:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
              |||:|||||   ||||||||:|||||   :::|||||||||||||||||||||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
              ||||||   ||||||   |||   |||   ||||:::|:||||   ||||:::|||:::||,
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTIGTGTACTGCTTTCGAAGAA 671
              |||   :::      ||||||||||||||||   |||   ||||||   ||||||:::
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
              |||||||||   |||   ||||||||||||||||||||||   |||   |||   ||||||

Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
              |||||||||      |||   ||||||   ||||||||   ::::||      |||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
              ||||||||||||   ||||||||||::::::   ::::::      |||:::||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
              ||||||||||||||||||||||||||||||||||||   |||||,|||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
              |||||||||||:::|||||||||||||||||||||||||||   |||||||||||:::
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              ||||||||||||||||||||||||||||||||||||   |||   ||||||:::||||||
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              ||||||||||||:::|||||||||||||||||||||||:::|||||||||:||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
              |||||||||   ::::::||||||   ||||||||||||||||||||||||||||||||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1152 TTGTCTACTACTTCTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              ||||||||||||:::|||||:::|||   :::|||||||||||||||||||||||||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              ||||||||||||:::|||   ||||||||||||||||||||||:::|||||||:::||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              ||||||||||||   ||||||   ||||||   ||||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
              :::|||   ||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467

RESULT 13
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
;  APPLICANT: Stafford, Christian F.
;  APPLICANT:  Trinci, Anthony P.J.
;  APPLICANT:  Brookman, Jayne L.
;  TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
;  TITLE OF INVENTION:  Phytase Enzymes and Vectors and Host Cells Incorporating Same
;  FILE REFERENCE: GC586-2
;  CURRENT APPLICATION NUMBER: US/10/229,358
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: US 60/148,960
;  PRIOR FILING DATE: 1999-08-13
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus niger
US-10-229-358-5
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Alignment Scores:

Pred. No.:	4.24e-142	Length:	467
Score:	1862.00	Matches:	348
Percent Similarity:	83.94%	Conservative:	44
Best Local Similarity:	74.52%	Mismatches:	75
Query Match:	73.74%	Indels:	0
DB:	15	Gaps:	0

US-09-488-265B-25 (1-1426) x US-10-229-358-5 (1-467)

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Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
              |||||||||      ||||||||  :::      |||  |||  |||||||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              |||:::            |||      ||||||||||||||||||   ||||||||||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
              |||   |||   ||||||||||||||||||||:::|||||||||||||||||:::|||
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
              |||   ||||||||:::||||||   ||||||||||||.||||   ||||.||| |||
Db         61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              ||||||||||||||||||||||||   |||||  ||||||||||||||||.|||| |||
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
              |||:||:::|||||||||   |||   ||||||||||||||||||||||||||||||:
Db        101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
              |||:::|||||||||||||||||||||||||||||:|||||:|:::::|||'||||||||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
              |||||||||||||:::|||||||:::::|||   |||   |||||||||||:::::|:::
Db        141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy        492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
              |||||||||   |||||:|||||||||   :::|||,|||||||||||,|||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
              ||||||   ||||||   |||   |||   |||:::|||||   ||:::|:|:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
              |||   :::      ||,|||||||||||||   |||   |:||||   ||||||:::
Db        201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
              |||||||||   |||   |||||||||||||||||||.||   |||   :||   .|||||
Db        221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
              |||||||||      |||   ||||||   ||||||||   :::|||      |||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
              ||||||||||||   |||||||||::::::   ::::::      ||||:::||||||||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
              ||||||||||||||||||||||||||||||||||   |||||||||||||||||||||
Db        281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
              ||||||||||||:::|||||||||||||||||||||||||   ||||||||||||:::
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        972 AACGAAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              ||||||.|||||||||||||||||||||||||||||:|||   |||  ||||||:::||||
Db        321 AsnGluIleIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              ||||||||||:|||:::|||||||||||||||||||||||:|:::|||:|||||||||||
Db        341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
              |||||||||   ::::::||||||   ||||||||||||||||||||||||||||.||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              |||||||||||||:::|||||||:::|||   :::|||||||||||||||||:::|||||
Db        381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||||||:::|||   ||||:|||||||||||||||:::|||||:::|||||||
Db        401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              |||||||||||||||||||||||||||||'||||||:|||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              ||,|||||||||   |,||||   ||||||   ||||||||:|||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
              :::|||   |||||||||||||
Db        461 AspTrpAlaGluCysPheAla 467
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RESULT 14
US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081355/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-929-060-3

Alignment Scores:

Pred. No.:	1.56e-141	Length:	467
Score:	1855.00	Matches:	343
Percent Similarity:	84.37%	Conservative:	51
Best Local Similarity:	73.45%	Mismatches:	73
Query Match:	73.47%	Indels:	0
DB:	9	Gaps:	0

US-09-488-265B-25 (1-1426) x US-09-929-060-3 (1-467)

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Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
              |||||||||      |||||||||  :::      |||  |||  |||||||||
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```
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              |||:::           |||      :::|||||||| ||||||   ||||||||:||||
Db         21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
              |||   |||   |||||||||||||||||||:|:::|||||||:|||||||||||:::::
Db         41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnLys 60

Qy        192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTGTCT 251
              |||||||||||||||||:|||||||   ||||||  ||||||||'   '|:||||:||||
Db         61 SerAlaIleSerProAspValProAlaGlyCysHisValThrPheAlaGlnValLeuSer 80

Qy        252 AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
              |||||||||||||||:||||:||||   ||:|||   |||||||||||.|||||:||||.|
Db         81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100

Qy        312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 371
              ||||||:::|||||||    |||:::|||:|||||||||||||||:|||  :|||
Db        101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLysThrTyrAsn 120

Qy        372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAACAAATGGTTAACTCTGGT 431
              |||:::|||||.|||'|.|||:|||||||||||||||'|.:::::||||:|||||'||
Db        121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

Qy        432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCGTTAGAGCT 491
              :::|||||||||::|||||||:::::|||   |||   ||||||||||:::::.|:::
Db        141 ValLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

Qy.       492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT 551
              ||||||||   ||||||||||||||      ||||||||||||||'|||||||||
Db        161 SerGlySerSerArgValIleAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThr 180

Qy        552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT 611
              ||||||   ||||||   |||   |||   |||:::|||||   |||:::|||:::|||
Db        181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

Qy        612 CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA 671
              |||   :::      ||||||||||||||||   .||   ||||||   ||.|||:::
Db        201 SerGluAlaSerThrSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220

Qy        672 TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
              ||||||||   |||'||:::|||||||||||||||||||   |||   |||   ||||||
Db        221 SerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

Qy        732 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG 791
              |||||||||      |||   ||||||:::|||||||||   :::|||      |'||
Db        241 GlnArgLeuGluAsnAspLeuSerGlyValSerLeuThrAspThrGluValThrTyrLeu 260

Qy        792 ATGGACATGTGTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA 851
              ||||||||||||   |||||'|||::::::   ::::::      |||:::||||||.|||
Db        261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

Qy        852 TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT 911
              |||||||||||||||||||:|||:::,|||||,||   ,|||||||||||'|||||  |||
Db        281 PheCysAspLeuPheThrHisGluGluTrpIleAsnTyrAspTyrLeuGlnSerLeuAsn 300

Qy        912 AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT 971
              ||||||||,|||::|||||||||||||||||||||'   || ||||||:|||:::
Db        301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320

Qy        972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC 1031
              |||||||||||||||||||||||||||||||:||||   |||   ||||||:::|||.'|
Db        321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340

Qy       1032 ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT 1091
              |||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

Qy       1092 CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA 1151
              |||||||||   :::::::||||||   ||||||||||||||||||||||||||,||||'||
Db        361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

Qy       1152 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAACTGACGGTTACGCTGCTTCTTGGACT 1211
              ||:|||:::|||:::   |||:::|||   :::|||||||||||:::::|||||
Db        381 LeuSerSerThrThrAlaGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

Qy       1212 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA 1271
              |||||||||||':::|||   ||||||||||||||||||||:::::|.|:::|||||
Db        401 ValProPheAlaSerArgMetTyrValGluMetMetGlnCysGlnSerGluGlnGluPro 420

Qy       1272 TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTTGACAAG 1331
              |||||||'||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

Qy       1332 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1391
              |||:|||||||||   |.||||   |||||||:::|||||||||||||||||||||||||
Db        441 LeuGlyArgCysThrArgAspSerPheValLysGlyLeuSerPheAlaArgSerGlyGly 460

Qy       1392 AACTGGGAAGAATGTTTCGCT 1412
              :::|||   ||||||||||||
Db        461 AspTrpGlyGluCysPheAla 467

RESULT 15
US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
;  APPLICANT: Svendsen, Allan
;  TITLE OF INVENTION: Phytase Variants
;  FILE REFERENCE: 5618.500-US
;  CURRENT APPLICATION NUMBER: US/10/083,452
;  CURRENT FILING DATE:  2002-02-26
;  PRIOR APPLICATION NUMBER: US/09/273,871
;  PRIOR FILING DATE: 1999-03-22
;  PRIOR APPLICATION NUMBER: PA 1998 00407
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: PA 1998 00806
;  PRIOR FILING DATE: 1998-06-19
;  PRIOR APPLICATION NUMBER: PA 1998 01176
;  PRIOR FILING DATE: 1998-09-18
;  PRIOR APPLICATION NUMBER: PA 1999 00091
;  PRIOR FILING DATE: 1999-01-22
;  PRIOR APPLICATION NUMBER: 60/080,129
;  PRIOR FILING DATE: 1998-03-31
;  PRIOR APPLICATION NUMBER: 60/090,675
;  PRIOR FILING DATE: 1998-06-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 467
;   TYPE: PRT
;   ORGANISM: Aspergillus ficuum
US-10-083-452-11

Alignment Scores:
Pred. No.:              3.97e-141       Length:         467
Score:                  1850.00         Matches:        346
Percent Similarity:     83.51%          Conservative:   44
Best Local Similarity:  74.09%          Mismatches:     77
Query Match:            73.27%          Indels:         0
DB:                     14              Gaps:           0

US-09-488-265B-25 (1-1426) x US-10-083-452-11 (1-467)

Qy         12 ATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC 71
              :'||||||||      |||||||||   :::      |||   |||   ||||'||||
Db          1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20

Qy         72 GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 131
              |||:::           |||      :::|||||||| ||||||   ||||||||:||||
Db         21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

Qy        132 TTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTTTGGCTGACGAA 191
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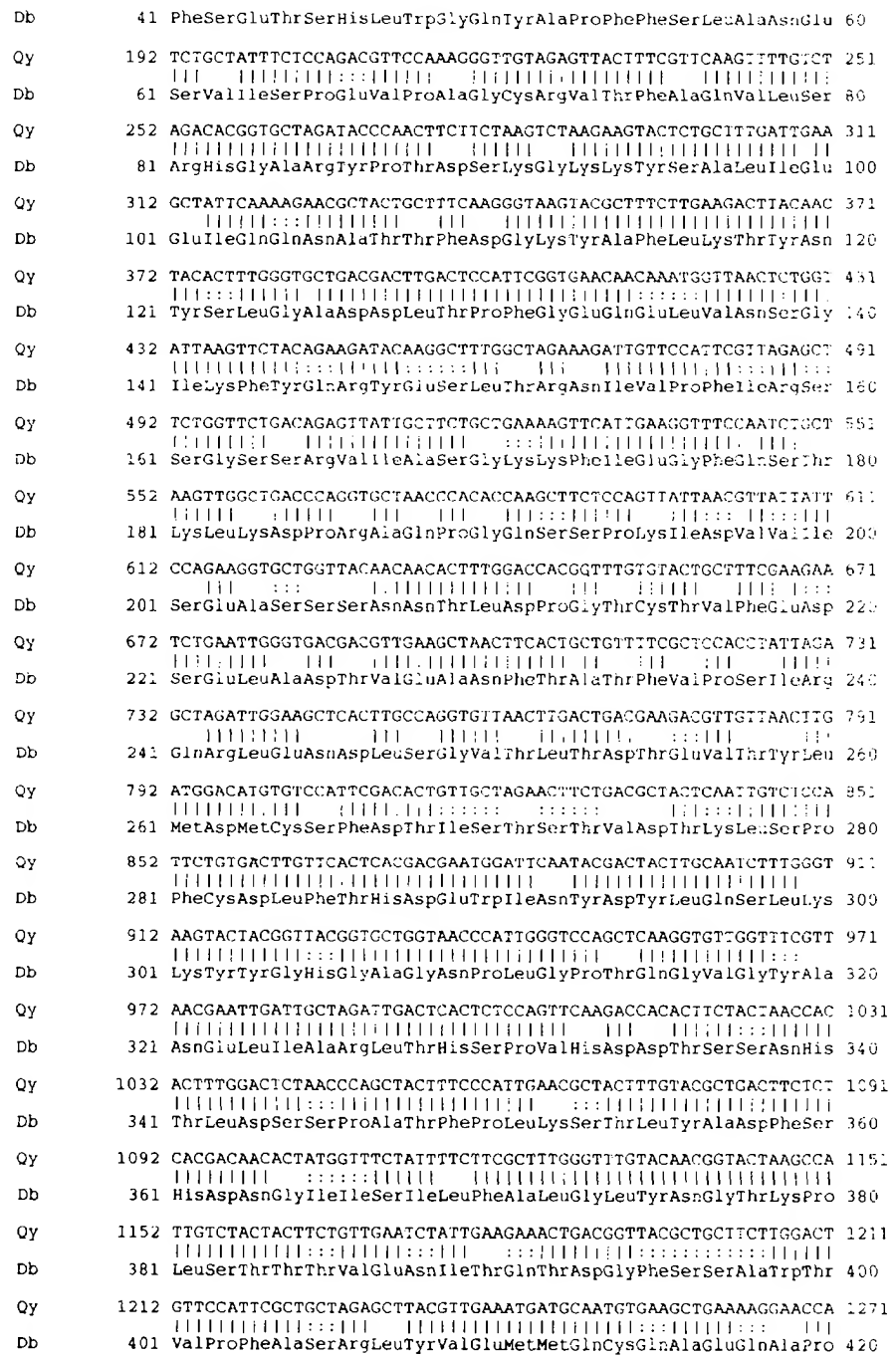

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